



## SEQUENCE LISTING

<110> Wonderling, Ramani S.  
Boroughs, Karen L.

<120> CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES  
THEREOF

<130> IM-5

<140> 09/917,265  
<141> 2001-07-27

<150> 60/223,016  
<151> 2000-08-04

<160> 111

<170> PatentIn version 3.2

<210> 1  
<211> 514  
<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
<222> (114)..(512)

<220>  
<221> misc\_feature  
<222> (470)..(470)  
<223> n = unknown at position 470  
Xaa = unknown at position 119

<400> 1  
gctaaaggcg ctccctgccac ctctctggcat ctacacagct cagaaaaaga aaggacacc 60

aaaccttcca gatcccttcc tctcttagga aactatttag cacaggata aag atg 116  
Met  
1

act gct ata cca gta gat gat tgc atc aac ttt gtg gga atg aaa ttt 164  
Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys Phe  
5 10 15

att gac aat aca ctt tac ttt gta gct gac agt gat gaa aac ctg gaa 212  
Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu Glu  
20 25 30

aca gat tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac 260  
Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn  
35 40 45

ttg aac gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt 308  
Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe

50	55	60	65	
gag gat atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu				356
70		75	80	
ttt atc ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val				404
85		90	95	
acc atc tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn				452
100		105	110	
aaa att att tcc ttt aan gga atg agt cct cct gag agt atc aat gat Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn Asp				500
115		120	125	
gaa gga aat gac at Glu Gly Asn Asp				514
130				
<210> 2				
<211> 133				
<212> PRT				
<213> Felis catus				
<220>				
<221> misc_feature				
<222> (119)..(119)				
<223> The 'Xaa' at location 119 stands for Lys, or Asn.				
<400> 2				
Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys				
1	5	10	15	
Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu				
20		25	30	
Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg				
35		40	45	
Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val				
50		55	60	
Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr				
65		70	75	80
Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala				
85		90	95	

Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu  
100 105 110

Asn Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn  
115 120 125

Asp Glu Gly Asn Asp  
130

<210> 3  
<211> 514  
<212> DNA  
<213> Felis catus

<220>  
<221> misc\_feature  
<222> (45)..(45)  
<223> n = unknown at position 45

<400> 3  
atgtcatttc ctcatcatt gatactctca ggaggactca ttccnttaaa ggaaataatt 60  
ttgttctcac aggagagagt agacatggtc ttataattca cagagatggt tactgccaga 120  
cctctagtga ggctatctt atacatataat atgataaatt cagtcgggg tgcattatct 180  
gtacagtcag aatcaggcat atcctcaaac acaggttgat ctccctgggt aatgaagaga 240  
acttggtcgt tcaagttcg taagatttag agtttatgtt caagcttgcc aaagtaatct 300  
gttccaggt tttcatcact gtcagctaca aagtaaagtg tattgtcaat aaatttcatt 360  
cccacaaagt tgatgcaatc atctactggt atagcagtca tctttatccc tgtgctcaat 420  
agttcctaa gagaggaagg gatctggaag gtttgaggtc cttttttt cctgagctgt 480  
gtagatggca gaaggtggca ggagcgcctt tagc 514

<210> 4  
<211> 502  
<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
<222> (3)..(464)

<220>  
<221> misc\_feature

<222> (126)..(126)

<223> n = unknown at position 126

Xaa = unknown at position 42

<400> 4

gc aag ctt gaa cat aaa ctc tca atc tta cga aac ttg aac gac caa 47  
Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln  
1 5 10 15

gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat atg cct 95  
Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro  
20 25 30

gat tct gac tgt aca gat aat gca ccc cgg nct gaa ttt atc ata tat 143  
Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr  
35 40 45

atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc tct gtg 191  
Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val  
50 55 60

aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att att tcc 239  
Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser  
65 70 75

ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga aat gac 287  
Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp  
80 85 90 95

atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag ata caa 335  
Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln  
100 105 110

ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa aaa gag 383  
Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu  
115 120 125

aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat ggg gat 431  
Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Asp Glu Asn Gly Asp  
130 135 140

aag tcc ata atg ttc act gtt caa aac aag aat tagatattaa aattgcataa 484  
Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn  
145 150

tttgaaaaaa aaaaaaaaaa 502

<210> 5

<211> 154

<212> PRT

<213> Felis catus

<220>

<221> misc\_feature

<222> (42)..(42)

<223> The 'Xaa' at location 42 stands for Thr, Ala, Pro, or Ser.

<400> 5

Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val  
1 5 10 15

Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp  
20 25 30

Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr Met  
35 40 45

Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn  
50 55 60

Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe  
65 70 75 80

Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile  
85 90 95

Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe  
100 105 110

Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys  
115 120 125

Asp Leu Phe Lys Leu Ile Leu Lys Lys Asp Glu Asn Gly Asp Lys  
130 135 140

Ser Ile Met Phe Thr Val Gln Asn Lys Asn  
145 150

<210> 6  
<211> 502  
<212> DNA  
<213> Felis catus

<220>  
<221> misc\_feature  
<222> (377)..(377)  
<223> n = unknown at position 377

<400> 6  
ttttttttt ttttcaaattt atgcaatttt aatatctaat tcttgaaaaaac aacagtgaac 60

attatggact tatccccatt ttcatcctt ttttcaaaa tgagttgaa aagatcttc	120
tcttttcac aagctagaaa gtacccttg tacaatgaag actcaaattg tatcttatca	180
tcatgtcctg gaacacttct ctgaaagaat atgatgtcat ttccttcattc attgatactc	240
tcaggaggac tcatttcctt aaaggaaata attttgttct cacaggagag agtagacatg	300
gtcttataat tcacagagat gttactgcc agacctctag tgaggctatc tttatacata	360
tatatgataa attcagnccg ggggcattt tctgtacagt cagaatcagg catatcctca	420
aacacaggtt gatctccctg gttaatgaag agaacttggc cgttcaagtt tcgtaagatt	480
gagagtttat gttcaagctt gc	502

<210> 7  
 <211> 607  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (24) .. (599)

<400> 7	
aactattttag cacaggata aag atg act gct ata cca gta gat gat tgc atc	53
Met Thr Ala Ile Pro Val Asp Asp Cys Ile	
1              5                 10	
aac ttt gtg gga atg aaa ttt att gac aat aca ctt tac ttt gta gct	101
Asn Phe Val Gly Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala	
15            20                 25	
gac agt gat gaa aac ctg gaa aca gat tac ttt ggc aag ctt gaa cat	149
Asp Ser Asp Glu Asn Leu Glu Thr Asp Tyr Phe Gly Lys Leu Glu His	
30            35                 40	
aaa ctc tca atc tta cga aac ttg aac gac caa gtt ctc ttc att aac	197
Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asn	
45            50                 55	
cag gga gat caa cct gtg ttt gag gat atg cct gat tct gac tgt aca	245
Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp Ser Asp Cys Thr	
60            65                 70	
gat aat gca ccc cgg act gaa ttt atc ata tat atg tat aaa gat agc	293
Asp Asn Ala Pro Arg Thr Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser	
75            80                 85                 90	
ctc act aga ggt ctg gca gta acc atc tct gtg aat tat aag acc atg	341
Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn Tyr Lys Thr Met	
95            100                 105	
tct act ctc tcc tgt gag aac aaa att att tcc ttt aag gaa atg agt	389

Ser	Thr	Leu	Ser	Cys	Glu	Asn	Lys	Ile	Ile	Ser	Phe	Lys	Glu	Met	Ser	
110								115						120		
cct	cct	gag	agt	atc	aat	gat	gaa	gga	aat	gac	atc	ata	ttc	ttt	cag	
Pro	Pro	Glu	Ser	Ile	Asn	Asp	Glu	Gly	Asn	Asp	Ile	Ile	Phe	Phe	Gln	
125								130						135		
aga	agt	gtt	cca	gga	cat	gat	gat	aag	ata	caa	ttt	gag	tct	tca	ttg	
Arg	Ser	Val	Pro	Gly	His	Asp	Asp	Lys	Ile	Gln	Phe	Glu	Ser	Ser	Leu	
140								145						150		
tac	aag	ggg	tac	ttt	cta	gct	tgt	gaa	aaa	gag	aaa	gat	ctt	ttc	aaa	
Tyr	Lys	Gly	Tyr	Phe	Leu	Ala	Cys	Glu	Lys	Glu	Lys	Asp	Leu	Phe	Lys	
155								160						170		
ctc	att	ttg	aaa	aaa	aag	gat	gaa	aat	ggg	gat	aag	tcc	ata	atg	ttc	
Leu	Ile	Leu	Lys	Lys	Asp	Glu	Asn	Gly	Asp	Lys	Ser	Ile	Met	Phe		
														175	180	185
act	gtt	caa	aac	aag	aat	tagatatt										607
Thr	Val	Gln	Asn	Lys	Asn											
						190										
<210>	8															
<211>	192															
<212>	PRT															
<213>	Felis catus															
<400>	8															
Met	Thr	Ala	Ile	Pro	Val	Asp	Asp	Cys	Ile	Asn	Phe	Val	Gly	Met	Lys	
1									10						15	
Phe	Ile	Asp	Asn	Thr	Leu	Tyr	Phe	Val	Ala	Asp	Ser	Asp	Glu	Asn	Leu	
20								25						30		
Glu	Thr	Asp	Tyr	Phe	Gly	Lys	Leu	Glu	His	Lys	Leu	Ser	Ile	Leu	Arg	
35								40						45		
Asn	Leu	Asn	Asp	Gln	Val	Leu	Phe	Ile	Asn	Gln	Gly	Asp	Gln	Pro	Val	
50								55						60		
Phe	Glu	Asp	Met	Pro	Asp	Ser	Asp	Cys	Thr	Asp	Asn	Ala	Pro	Arg	Thr	
65								70						80		
Glu	Phe	Ile	Ile	Tyr	Met	Tyr	Lys	Asp	Ser	Leu	Thr	Arg	Gly	Leu	Ala	
85								90						95		
Val	Thr	Ile	Ser	Val	Asn	Tyr	Lys	Thr	Met	Ser	Thr	Leu	Ser	Cys	Glu	
100								105						110		

Asn Lys Ile Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn  
115 120 125

Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His  
130 135 140

Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu  
145 150 155 160

Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys  
165 170 175

Asp Glu Asn Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn  
180 185 190

<210> 9  
<211> 576  
<212> DNA  
<213> Felis catus

<400> 9  
atgactgcta taccagtaga tgattgcata aactttgtgg gaatgaaatt tattgacaat 60  
acactttact ttgttagctga cagtgtatgaa aacctggaaa cagattactt tggcaagctt 120  
gaacataaac tctcaatctt acgaaacttg aacgaccaag ttctcttcata taaccaggaa 180  
gatcaacctg tgtttgagga tatgcctgat tctgactgta cagataatgc accccggact 240  
gaatttatca tatatatgta taaagatagc ctcactagag gtctggcagt aaccatctct 300  
gtgaattata agaccatgtc tactctctcc tgtgagaaca aaattatttc cttaaggaa 360  
atgagtcctc ctgagagttt caatgtatgaa ggaaatgaca tcataattttt tcagagaagt 420  
gttccaggac atgatgataa gatacaattt gagtcttcata tgtacaaggg gtactttctta 480  
gcttgtgaaa aagagaaaaga tcctttcaaa ctcattttga aaaaaaaagga tgaaaatggg 540  
gataagtcca taatgttcac tggcaaaac aagaat 576

<210> 10  
<211> 607  
<212> DNA  
<213> Felis catus

<400> 10  
aatatctaat tcttgtttg aacagtgaac attatggact tatccccatt ttcatccttt 60

ttttcaaaa	tgagttgaa	aagatcttc	tctttcac	aagctagaaa	gtacccttg	120
tacaatgaag	actcaaattg	tatcttatca	tcatgcctg	gaacacttct	ctgaaagaat	180
atgatgtcat	ttccttcatc	attgatactc	tcaggaggac	tcatttcctt	aaaggaaata	240
atttgttct	cacaggagag	agtagacatg	gtcttataat	tcacagagat	ggttactgcc	300
agacctctag	tgaggctatc	tttatacata	tatatgataa	attcagtccg	gggtgcatta	360
tctgtacagt	cagaatcagg	catatcctca	aacacagggtt	gatctccctg	gttaatgaag	420
agaacttgg	cgttcaagtt	tcgtaagatt	gagagtttat	gttcaagctt	gccaaagtaa	480
tctgtttcca	ggttttcatc	actgtcagct	acaaagtaaa	gtgtattgtc	aataaatttc	540
atcccacaa	agttgatgca	atcatctact	ggtatagcag	tcatctttat	ccctgtgctc	600
aatagtt						607

<210> 11  
<211> 471  
<212> DNA  
<213> Felis catus

<220>						
<221>	CDS					
<222>	(1)..(471)					
<400> 11						
tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac ttg aac						48
Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn						
1	5	10	15			
gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat						96
Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp						
20	25	30				
atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa ttt atc						144
Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile						
35	40	45				
ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc						192
Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile						
50	55	60				
tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att						240
Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile						
65	70	75	80			
att tcc ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga						288
Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly						
85	90	95				
aat gac atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag						336

Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys			
100	105	110	
ata caa ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa			384
Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu			
115	120	125	
aaa gag aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat			432
Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Asp Glu Asn			
130	135	140	
ggg gat aag tcc ata atg ttc act gtt caa aac aag aat			471
Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn			
145	150	155	
<210> 12			
<211> 157			
<212> PRT			
<213> Felis catus			
<400> 12			
Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn			
1	5	10	15
Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp			
20	25	30	
Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile			
35	40	45	
Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile			
50	55	60	
Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile			
65	70	75	80
Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly			
85	90	95	
Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys			
100	105	110	
Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu			
115	120	125	
Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Asp Glu Asn			
130	135	140	

Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn  
145 150 155

<210>	13
<211>	471
<212>	DNA
<213>	<i>Felis catus</i>

<400> 13 attcttggttt tgaacagtga acattatgga cttatccccca ttttcatcct ttttttcaa 60  
aatagagtttggaaaagatctttctctcttttcacaagctaga aagtacccttgtacaatga 120  
agactcaaataatgttatcatcatgtcc tgaaacactt ctctgaaaga atatgatgtc 180  
atttccttca tcattgatacttcaggagg actcatttcc ttAAAGGAAA taattttgtt 240  
ctcacaggag agagtagaca tggtcttata attcacagag atggttactg ccagacctct 300  
agtggggcta tctttataca tatatatgtt aaattcagtc cggggtgcat tatctgtaca 360  
gtcagaatca ggcataatcct caaacacagg ttgatctccc tggttaatga agagaacttg 420  
gtcggttcaag tttcgtaaga ttgagagttt atgttcaagc ttgccaaagt a 471

```
<210> 14
<211> 1233
<212> DNA
<213> Felis catus
```

<220>  
<221> CDS  
<222> (1)..(1230)

```

<400> 14
atg gcc gac aag gtc ctg aag gag aag agg aag cag ttc atc aac tca      48
Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Gln Phe Ile Asn Ser
1           5           10           15

gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa      96
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
20          25          30

aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct      144
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
35          40          45

acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa      192
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
50          55          60

ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac      240

```

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp			
65	70	75	80
acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga			288
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly			
85	90	95	
aat tct cag aac acc acg gac tct gaa gta gcg ttt cct cct ctt cca			336
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro			
100	105	110	
gcc agc gtg aat aac atg cct ggg ccg gct gag cca gaa gaa tct gta			384
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val			
115	120	125	
gat gct ctc aag ctt tgt cct cgt gaa aac ttc gtg aaa ctg tgt aaa			432
Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys			
130	135	140	
cag agg gct gaa gag atc tac cca ata aag gag aga aag gat cgt act			480
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr			
145	150	155	160
cgt ctg gct ctc atc ata tgc aat acg acg ttc gat cat ctt tct ctc			528
Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu			
165	170	175	
agg aag ggg gct gac ctt gac gtt gca ggg atg agg agg ctg ctt aca			576
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr			
180	185	190	
gac ctt ggc tac agt gtg cac ata aaa gag gaa ctc act gct aag gac			624
Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp			
195	200	205	
atg gaa tca gag ctg agg gca ttt gct gcc cgt cca gag cac aag tcc			672
Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser			
210	215	220	
tcg gac agc aca ttc ctg gtg ttc atg tct cat ggc atc ctg agt gga			720
Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly			
225	230	235	240
atc tgt ggg acg aag tac agc gct gaa gga gac cca gat gta ttg gct			768
Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala			
245	250	255	
tat gac acc atc ttc cag att ttc aac aac cgc aac tgc ctt agt cta			816
Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu			
260	265	270	
aag gac aag ccc aag gtc atc atc gtc cag gcc tgc aga ggt gaa aat			864
Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn			
275	280	285	
ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc			912
Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser			

290

295

300

act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag 960  
 Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu  
 305 310 315 320

```

gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc      1008
Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
            325          330          335

```

tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga 1056  
 Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly  
           340              345              350

tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg 1104  
 Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp  
           355              360              365

tgc ttt cat ctg gag gaa gta ttt cg<sup>370</sup> aag gta caa cag tca ttt gaa 1152  
Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu  
370 375 380

```

aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg      1200
Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
385           390           395           400

```

aca aga tgt ttc tac ctc ttc cca gga cat taa 1233  
 Thr Arg Cys Phe Tyr Leu Phe Pro Gly His  
 405 410

<210> 15  
<211> 410  
<212> PRT  
<213> *Felis catus*

<400> 15

Met	Ala	Asp	Lys	Val	Leu	Lys	Glu	Lys	Arg	Lys	Gln	Phe	Ile	Asn	Ser
1				5					10					15	

Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys  
20 25 30

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala  
35 40 45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys  
50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp  
65                   70                   75                   80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly  
85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro  
100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val  
115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys  
130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr  
145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu  
165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr  
180 185 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp  
195 200 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser  
210 215 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly  
225 230 235 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala  
245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu  
260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn  
275 280 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser  
290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu  
305 310 315 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe  
325 330 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly  
340 345 350

Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp  
355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu  
370 375 380

Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met  
385 390 395 400

Thr Arg Cys Phe Tyr Leu Phe Pro Gly His  
405 410

<210> 16  
<211> 1233  
<212> DNA  
<213> Felis catus

<400> 16  
ttaatgcctt gggaaagaggt agaaaacatct tgtcatggat agtcgttcaa tgggtggcat 60  
ctgggctcta acattttggtt ttcaaatga ctgttgtacc ttccgaaata cttcctccag 120  
atggaaagcac cacgaataact ttggaaagca cgtgatgagt tgtgtaatga agagagatcc 180  
cttggttcacg tctctccaag acacatgatg tggggtcgag gagcagaaag cgatgaagtc 240  
cttctccacg tggaccttgt aaatggcgtc gtcctctagg ttgtcaccct cctgtgaaag 300  
gctgctaccc atctgtgaag tgctgtccat tggggccgct ggagagtcac tgatcaacag 360  
ttcccccaaa tttcacctc tgcaaggctg gacgatgatg accttggct tgccttttag 420  
actaaggcag ttgcgggtgt tgaaaatctg gaagatggtg tcataagcca atacatctgg 480  
gtctccttca gcgctgtact tcgtcccaca gattccactc aggatgccat gagacatgaa 540  
caccaggaat gtgctgtccg aggacttgtg ctctggacgg gcagcaaatg ccctcagctc 600  
tgattccatg tccttagcag tgagttcctc ttttatgtgc acactgttagc caaggctgt 660  
aaggcagcctc ctcatccctg caacgtcaag gtcagcccc ttcctgagag aaagatgatc 720

gaacgtcgta ttgcatatga tgagagccag acgagtacga tcctttctct cctttattgg	780
gtagatctct tcagccctct gtttacacag tttcacgaag ttttcacgag gacaaagctt	840
gagagcatct acagattctt ctggctcagc cgccccaggc atgttattca cgctggctgg	900
aagaggagga aacgctactt cagagtccgt ggtgttctga gaatttccag attgtggct	960
tgaggagagc cccagcgtct ctgcaagggtg ggtgtttcc tcacagatgt gacagataaa	1020
gatctggcac gcccgtggcc ctttccgcag gacgctgtcg atcagagctc gggccttgc	1080
cataacggta gcgtttcac attttactct ctccatctcc tcctggttca gcacgtttt	1140
ctcaaagagt tcatccagca agccgttgac cgtccccatg ccgactgagt tcatgaactg	1200
cttcctcttc tccttcagga ccttgcggc cat	1233

<210> 17  
<211> 526  
<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
<222> (18) .. (524)

<400> 17	
ggcacgagca aaaagcc atg gcc gac aag gat ctg aag ggc aag agg aag	50
Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys	
1              5                 10	
cag ttc atc aac tca gtc ggc atg ggg acg gtc aac ggc ttg ctg gat	98
Gln Phe Ile Asn Ser Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp	
15            20                25	
gaa ctc ttt gag aaa aac gtg ctg aac cag gag gag atg gag aga gta	146
Glu Leu Phe Glu Lys Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val	
30            35                40	
aaa tgt gaa aac gct acc gtt atg gac aag gcc cga gct ctg atc gac	194
Lys Cys Glu Asn Ala Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp	
45            50                55	
agc gtc ctg cgg aaa ggg cca cgg gcg tgc cag atc ttt atc tgt cac	242
Ser Val Leu Arg Lys Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His	
60            65                70                75	
atc tgt gag gaa gac acc cac ctt gca gag acg ctg ggg ctc tcc tca	290
Ile Cys Glu Glu Asp Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser	
80            85                90	
agc cca caa tct gga aat tct cag aac acc acg gac tct gaa gta gcg	338
Ser Pro Gln Ser Gly Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala	

95	100	105	
ttt cct cct ctt cca gcc agc gtg aat aac atg cct ggg ccg gct gag Phe Pro Pro Leu Pro Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu 110	115	120	386
cca gaa gaa tct gta gat gct ctc aag ctt tgt cct cgt gaa aac ttc Pro Glu Glu Ser Val Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe 125	130	135	434
gtg aaa ctg tgt aaa cag agg gct gaa gag atc tac cca ata aag gag Val Lys Leu Cys Lys Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu 140	145	150	482
aga aag gat cgt act cgt ctg gct ctc atc ata tgc aat acg ac Arg Lys Asp Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr 160	165		526
<210> 18			
<211> 169			
<212> PRT			
<213> Felis catus			
<400> 18			
Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser 1	5	10	15
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys 20	25	30	
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala 35	40	45	
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys 50	55	60	
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp 65	70	75	80
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly 85	90	95	
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro 100	105	110	
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val 115	120	125	

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys  
130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr  
145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr  
165

<210> 19  
<211> 526  
<212> DNA  
<213> Felis catus

<400> 19  
gtcgtaattgc atatgatgag agccagacga gtacgatcct ttctctcctt tattggtag 60  
atctcttcag ccctctgttt acacagttc acgaagttt cacgaggaca aagcttgaga 120  
gcatactacag attcttctgg ctcagccggc ccaggcatgt tattcacgct ggctggaaga 180  
ggagggaaacg ctacttcaga gtccgtggtg ttctgagaat ttccagattt tgggcttgag 240  
gagagccccca gcgtctctgc aaggtgggtg tcttcctcac agatgtgaca gataaagatc 300  
tggcacgccc gtggcccttt ccgcaggacg ctgtcgatca gagctcgggc cttgtccata 360  
acggtagcgt tttcacattt tactctctcc atctcctcct ggttcagcac gttttctca 420  
aagagttcat ccagcaagcc gttgaccgtc cccatgccga ctgagtttat gaactgcttc 480  
ctttgccct tcagatcctt gtcggccatg gcttttgct cgtgcc 526

<210> 20  
<211> 500  
<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
<222> (3)..(362)

<220>  
<221> misc\_feature  
<222> (473)..(473)  
<223> n = unknown at position 473

<400> 20  
gg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc act 47  
Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr  
1 5 10 15

tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag gac Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp	95
20 25 30	
gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc tgc Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys	143
35 40 45	
tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga tct Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser	191
50 55 60	
ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg tgc Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys	239
65 70 75	
ttt cat ctg gag gaa gta ttt cg <sup>g</sup> aag gta caa cag tca ttt gaa aaa Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys	287
80 85 90 95	
cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg aca Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr	335
100 105 110	
aga tac ttc tat ctc ttc cct ggc aat tgaaaatagc aatcatgggc Arg Tyr Phe Tyr Leu Phe Pro Gly Asn	382
115 120	
agtccagccc ttcttgacca acttgaaaaa gtaccttagc tagcacaaca cactcattta	442
acgtttggta tctcaataaa aatgaaaaca nctaaaaaaaaaaaaaaaaaaaaaaa	500
<210> 21	
<211> 120	
<212> PRT	
<213> Felis catus	
<400> 21	
Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr Ser	1
5 10 15	
Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp Asp	20 25 30
Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys Ser	35 40 45
Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser Leu	50 55 60

Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys Phe  
65 70 75 80

His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys Pro  
85 90 95

Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr Arg  
100 105 110

Tyr Phe Tyr Leu Phe Pro Gly Asn  
115 120

<210> 22  
<211> 500  
<212> DNA  
<213> Felis catus

<220>  
<221> misc\_feature  
<222> (28)..(28)  
<223> n = unknown at position 28

<400> 22  
ttttttttt tttttttttt ttttagntg ttttcatttt tattgagata ccaaacgtta 60  
aatgagtgtg ttgtgctagc taaggtactt ttccaagttg gtcaagaagg gctggactgc 120  
ccatgattgc tattttcaat tgccagggaa gagatagaag tatcttgtca tggatagtcg 180  
ttcaatggtg ggcatctggg ctctaacatt tggttttca aatgactgtt gtaccctccg 240  
aaatacttcc tccagatgaa agcaccacga atactttgg aagcacgtga tgagttgtgt 300  
aatgaagaga gatcccttgt tcacgtctct ccaagacaca tggatgtgggg tcgaggagca 360  
gaaagcgatg aagtccctct ccacgtggac cttgtaaatg gcgtcgtcct ctaggttgtc 420  
acccacctgt gaaaggctgc tacccatctg tgaagtgctg tccattgggg ccgctggaga 480  
gtcactgatc aacagttccc 500

<210> 23  
<211> 1230  
<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
<222> (1)..(1230)

<400> 23			
atg gcc gac aag gat ctg aag ggc aag agg aag cag ttc atc aac tca			48
Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser			
1 5 10 15			
gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa			96
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys			
20 25 30			
aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct			144
Asn Val Leu Asn Gln Glu Met Glu Arg Val Lys Cys Glu Asn Ala			
35 40 45			
acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgaa			192
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys			
50 55 60			
ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac			240
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp			
65 70 75 80			
acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga			288
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly			
85 90 95			
aat tct cag aac acc acg gac tct gaa gta gcg ttt cct cct ctt cca			336
Asn Ser Gln Asn Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro			
100 105 110			
gcc agc gtg aat aac atg cct ggg ccg gct gag cca gaa gaa tct gta			384
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val			
115 120 125			
gat gct ctc aag ctt tgt cct cgt gaa aac ttc gtg aaa ctg tgt aaa			432
Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys			
130 135 140			
cag agg gct gaa gag atc tac cca ata aag gag aga aag gat cgt act			480
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr			
145 150 155 160			
cgt ctg gct ctc atc ata tgc aat acg acg ttc gat cat ctt tct ctc			528
Arg Leu Ala Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu			
165 170 175			
agg aag ggg gct gac ctt gac gtt gca ggg atg agg agg ctg ctt aca			576
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr			
180 185 190			
gac ctt ggc tac agt gtg cac ata aaa gag gaa ctc act gct aag gac			624
Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp			
195 200 205			
atg gaa tca gag ctg agg gca ttt gct gcc cgt cca gag cac aag tcc			672
Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser			
210 215 220			

tcg gac agc aca ttc ctg gtg ttc atg tct cat ggc atc ctg agt gga		720	
Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly			
225	230	235	240
atc tgt ggg acg aag tac agc gct gaa gga gac cca gat gta ttg gct		768	
Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala			
245	250	255	
tat gac acc atc ttc cag att ttc aac aac cgc aac tgc ctt agt cta		816	
Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu			
260	265	270	
aag gac aag ccc aag gtc atc atc gtc cag gcc tgc aga ggt gaa aat		864	
Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn			
275	280	285	
ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc		912	
Leu Gly Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser			
290	295	300	
act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag		960	
Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu			
305	310	315	320
gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc		1008	
Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe			
325	330	335	
tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga		1056	
Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly			
340	345	350	
tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg		1104	
Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp			
355	360	365	
tgc ttt cat ctg gag gaa gta ttt cg <sup>g</sup> aag gta caa cag tca ttt gaa		1152	
Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu			
370	375	380	
aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg		1200	
Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met			
385	390	395	400
aca aga tac ttc tat ctc ttc cct ggc aat		1230	
Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn			
405	410		

<210> 24  
<211> 410  
<212> PRT  
<213> Felis catus

<400> 24

Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser

1 5 10 15

Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys  
20 25 30

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala  
35 40 45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys  
50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp  
65 70 75 80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly  
85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro  
100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val  
115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys  
130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr  
145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu  
165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr  
180 185 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp  
195 200 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser  
210 215 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly  
225 230 235 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala  
245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu  
260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn  
275 280 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser  
290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu  
305 310 315 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe  
325 330 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly  
340 345 350

Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp  
355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu  
370 375 380

Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met  
385 390 395 400

Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn  
405 410

<210> 25

<211> 1230

<212> DNA

<213> Felis catus

<400> 25

attgccaggg aagagataga agtatcttgt catggatagt cgttcaatgg tgggcacatcg 60

ggctctaaca tttgggtttt caaatgactg ttgtaccctc cgaaatactt cctccagatg 120

aaagcaccac gaatactttt ggaagcacgt gatgagttgt gtaatgaaga gagatccctt 180

gttcacgtct	ctccaagaca	catgatgtgg	ggtcgaggag	cagaaagcga	tgaagtccctt	240
ctccacgtgg	accttgtaaa	tggcgctgac	ctctaggttg	tcacccaccc	gtgaaaggct	300
gctaccatc	tgtgaagtgc	tgtccattgg	ggccgctgga	gagtcactga	tcaacagttc	360
ccccaaattt	tcacacctgc	aggcctggac	gatgatgacc	ttgggcttgt	ccttttagact	420
aaggcagttg	cgggttgtga	aaatctggaa	gatgggtgtca	taagccaata	catctgggtc	480
tccttcagcg	ctgtacttcg	tcccacagat	tccactcagg	atgccatgag	acatgaacac	540
caggaatgtg	ctgtccgagg	acttgtgctc	tggacgggca	gcaaattgccc	tcagctctga	600
ttccatgtcc	ttagcagtga	gttcctctt	tatgtgcaca	ctgtagccaa	ggtctgttaag	660
cagcctcctc	atccctgcaa	cgtcaaggtc	agcccccttc	ctgagagaaa	gatgatcgaa	720
cgtcgttattg	catatgatga	gagccagacg	agtacgatcc	tttctctcct	ttattgggta	780
gatctttca	gccctctgtt	tacacagttt	cacgaagttt	tcacgaggac	aaagcttgag	840
agcatctaca	gattcttctg	gctcagccgg	cccaggcatg	ttattcacgc	tggctgaaag	900
aggagggaaac	gctacttcag	agtccgtgg	gttctgagaa	tttccagatt	gtgggcttga	960
ggagagcccc	agcgtctctg	caaggtgggt	gttttcctca	cagatgtgac	agataaagat	1020
ctggcacgcc	cgtggccctt	tccgcaggac	gctgtcgatc	agagctcggg	ccttgcctat	1080
aacggtagcg	ttttcacatt	ttactctctc	catctcctcc	tggttcagca	cgttttctc	1140
aaagagttca	tccagcaagc	cgttgaccgt	ccccatgccc	actgagttga	tgaactgctt	1200
cctcttgccc	ttcagatcct	tgtcgccat				1230

<210> 26  
 <211> 921  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(921)

<400> 26						
ata tgg gaa ctg gag aaa aac gtt tat gtt gta gag ttg gac tgg cac						48
Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His						
1	5	10	15			
cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa						96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu						
20	25	30				

gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc		144	
Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly			
35	40	45	
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc		192	
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly			
50	55	60	
cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc		240	
Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu			
65	70	75	80
ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg		288	
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg			
85	90	95	
gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag		336	
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys			
100	105	110	
aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg gca atc agt acc		384	
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr			
115	120	125	
gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa		432	
Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln			
130	135	140	
gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg		480	
Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val			
145	150	155	160
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt		528	
Asp Asn Arg Asp Tyr Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser			
165	170	175	
gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac		576	
Ala Cys Pro Ala Ala Glu Ser Leu Pro Ile Glu Val Val Val Asp			
180	185	190	
gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc		624	
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile			
195	200	205	
agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca		672	
Arg Asp Ile Ile Lys Pro Asp Pro Lys Asn Leu Gln Leu Lys Pro			
210	215	220	
tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc		720	
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr			
225	230	235	240
tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc		768	
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val			
245	250	255	
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag		816	

Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Asp	Arg	Leu	Ser	Val	Asp	Lys		
260						265							270			
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	864
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	
275						280							285			
gcc	aga	gac	cgc	tac	tat	agc	tca	tcc	tgg	agc	aac	tgg	gca	tcc	gtg	912
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Trp	Ser	Asn	Trp	Ala	Ser	Val		
290						295							300			
tcc	tgc	agt													921	
Ser	Cys	Ser														
305																
<210>	27															
<211>	307															
<212>	PRT															
<213>	Felis catus															
<400>	27															
Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val	Val	Glu	Leu	Asp	Trp	His	
1							5				10				15	
Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	Thr	Cys	Asn	Thr	Pro	Glu	
							20				25				30	
Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln	Ser	Ser	Glu	Val	Leu	Gly	
							35				40				45	
Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	Glu	Phe	Ala	Asp	Ala	Gly	
							50				55				60	
Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val	Leu	Ser	His	Ser	Phe	Leu	
							65				70				75	80
Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	Ser	Thr	Asp	Ile	Leu	Arg	
							85				90				95	
Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys	
							100				105				110	
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr	
							115				120				125	
Asp	Leu	Lys	Phe	Thr	Val	Lys	Ser	Ser	Arg	Gly	Ser	Ser	Asp	Pro	Gln	
							130				135				140	

Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val  
145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser  
165 170 175

Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp  
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile  
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro  
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr  
225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val  
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys  
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln  
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val  
290 295 300

Ser Cys Ser  
305

<210> 28  
<211> 921  
<212> DNA  
<213> Felis catus

<400> 28  
actgcaggac acggatgccc agttgctcca ggatgagcta tagtagcggt ctctggcttg 60  
cacgcggatc ttggcatcct tgtggcacac gacctggct gaggtcttgt ccacggagag 120  
tctgtcttcc ttttctctgt tggtcttgcc ctggacctgt acgccaaatg ttaaggagaa 180

gtaggaatgt	gggggtgctcc	agggtgcagg	gtattcccag	ctcaacttcca	catgccgaga	240
attttttaat	ggcttcagtt	gcaggttctt	gggtgggtcc	ggtttgatga	tgtccctgat	300
gaagaagctg	ctgggttagt	tttcgtactt	gagcttgtga	atagcgtcca	ccacgacttc	360
aatgggttagg	cttcctcg	cagccgggca	ggcactgccc	tcctgacact	ccactgtgta	420
cttcttataa	tccctgttgt	ccactctgac	cttctctgct	gagagtgtcg	ctgctccaca	480
agtcacctct	tgggggtcag	aggagcctct	gctgctttg	acagtgaatt	tcaaatcggt	540
actgattgcc	gtcagccacc	agcaggtgaa	acgtccagaa	taattcttg	cctcacattt	600
tagaaagatc	ttatTTTgg	attcttctg	ttcccttaag	atatcagtgg	accaaattcc	660
atttccctt	ttgtgtatca	ggaggaacga	atggctcaga	acctcgcc	ctttatgaca	720
ggtatactgg	ccagcatctg	caaattctt	gacttggatg	gtcagagtt	taccagagcc	780
taggacttca	ctgctctggt	cagaggtcca	ggtgatgtca	tcttcttcag	gagtattgca	840
ggtgaggacc	accatttctc	cggggc	agggtgccag	tccaactcta	caacataaaac	900
gttttctcc	agttcccata	t				921

<210> 29  
 <211> 987  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(987)

<400> 29	
atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg	48
Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu	
1 5 10 15	
gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt	96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val	
20 25 30	
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc	144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag	192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln	
50 55 60	
agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa	240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	

65	70	75	80	
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val 85 90 95				288
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp 100 105 110				336
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe 115 120 125				384
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp 130 135 140				432
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg 145 150 155 160				480
ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser 165 170 175				528
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtc Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val 180 185 190				576
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro 195 200 205				624
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac Ile Glu Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210 215 220				672
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys 225 230 235 240				720
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245 250 255				768
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260 265 270				816
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275 280 285				864
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290 295 300				912

gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg		960	
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp			
305	310	315	320
agc aac tgg gca tcc gtg tcc tgc agt		987	
Ser Asn Trp Ala Ser Val Ser Cys Ser			
325			
<210> 30			
<211> 329			
<212> PRT			
<213> Felis catus			
<400> 30			
Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu			
1	5	10	15
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val			
20	25	30	
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu			
35	40	45	
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln			
50	55	60	
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys			
65	70	75	80
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val			
85	90	95	
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp			
100	105	110	
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe			
115	120	125	
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp			
130	135	140	
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg			
145	150	155	160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser  
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro  
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser  
325

<210> 31  
<211> 987  
<212> DNA  
<213> Felis catus

<400> 31  
actgcaggac acggatgccc agttgctcca ggatgagcta tagtagcggt ctctggcttg 60  
cacgcggatc ttggcatcct tgtggcacac gacctggct gaggtcttgt ccacggagag 120  
tctgtcttc ttttctctgt ttttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180  
gttaggaatgt ggggtgctcc aggtgtcagg gtattccag ctcacttcca catgccgaga 240

atttttaat ggcttcagtt gcaggttctt gggtagatgc tgccctgat	300
gaagaagctg ctgggtgtactt gagcttgtga atagcgtcca ccacgacttc	360
aatgggttagg ctctcctcgg cagccgggca ggcactgccc tcctgacact ccactgtgta	420
cttcttataa tccctgttgc ccactctgac cttcttgct gagagtgtcg ctgctccaca	480
agtccccct tgggggtcag aggaggctct gctgctttg acagtgaatt tcaaatcggt	540
actgattgcc gtcagccacc agcaggtgaa acgtccagaa taattcttg ctcacattt	600
tagaaagatc ttatTTTgg attcttctg ttcccttaag atatcagtgg accaaattcc	660
atcttccttt ttgtgtatca ggaggaacga atggctcaga acctcgccctc ctatgaca	720
ggtatactgg ccagcatctg caaattctt gacttggatg gtcagagttt taccagagcc	780
taggacttca ctgctctggc cagaggtcca ggtgatgtca tcttcttcag ggttattgca	840
ggtgaggacc accatttctc cgggggcattc agggtgccag tccaaactcta caacataaac	900
gttttctcc agttccata tggccatgag gggaggtgcc agcaaaacca gggaaaacca	960
ggcgatgacc aactgctgag gatgcat	987

<210> 32  
 <211> 666  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(666)

atg tgc ccg ccg cgt ggc ctc ctc ctt gta acc atc ctg gtc ctg tta	48
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu	
1 5 10 15	
aac cac ctg gac cac ctc agt ttg gcc agg aac ctc ccc aca ccc aca	96
Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr	
20 25 30	
cca agc cca gga atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg	144
Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu	
35 40 45	
cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa ttt	192
Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe	
50 55 60	
tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa gat	240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp	

65	70	75	80	
aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn 85 90 95				288
gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg agt Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser 100 105 110				336
tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser 115 120 125				384
agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met 130 135 140				432
aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln 145 150 155 160				480
aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc aac Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn 165 170 175				528
agt gtg act gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr 180 185 190				576
aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg 195 200 205				624
gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser 210 215 220				666
<210> 33				
<211> 222				
<212> PRT				
<213> Felis catus				
<400> 33				
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu 1 5 10 15				
Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr 20 25 30				
Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu 35 40 45				

Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe  
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp  
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn  
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser  
100 105 110

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser  
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met  
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln  
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn  
165 170 175

Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr  
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg  
195 200 205

Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser  
210 215 220

<210> 34  
<211> 666  
<212> DNA  
<213> Felis catus

<400> 34  
ggaaggattc agatagctca tcattctatt gatggtaact gcacgaattc tgaaagcatg 60  
aagaagtatg cagagcttga ttttagttt ataaaaatcc ggttcttcca gggaggagtt 120  
ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180

catgtttga tccagaaaaga tctgcctttt aggatccatt aacagcttg cattcatggc	240
cttgaactcc acctggtaca tcttcaggta ctcataagata ctgctaaggc acagggtcgt	300
cataaaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctct	360
ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct	420
ggtttatct tttgtgatat ctcatgatc aatctttcg gaagtgcagg agtaaaattc	480
tagagttgt ctggccttct gaagcgtgtt gctgatggct cgccaggcagg tttggagtg	540
gttggggcac tggaacattc ctgggcttgg tgtgggtgtg gggaggttcc tggccaaact	600
gaggtggtcc aggtggttta acaggaccag gatggttaca aggaggaggc cacgcggcgg	660
gcacat	666

<210> 35  
<211> 591  
<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
<222> (1)..(591)

<400> 35	
agg aac ctc ccc aca ccc aca cca agc cca gga atg ttc cag tgc ctc	48
Arg Asn Leu Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu	
1 5 10 15	
aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag	96
Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys	
20 25 30	
gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat	144
Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp	
35 40 45	
cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta	192
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	
50 55 60	
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc	240
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	
65 70 75 80	
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt	288
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe	
85 90 95	
atg acg acc ctg tgc ctt agc agt atc tat gag gac ttg aag atg tac	336
Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr	
100 105 110	

cag gtg gag ttc aag gcc atg aat gca aag ctg tta atg gat cct aaa		384
Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys		
115	120	125
agg cag atc ttt ctg gat caa aac atg ctg aca gct att gat gag ctg		432
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu		
130	135	140
tta cag gcc ctg aat gtc aac agt gtg act gtg cca cag aac tcc tcc		480
Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser		
145	150	155
160		
ttg gaa gaa ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt		528
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu		
165	170	175
ctt cat gct ttc aga att cgt gca gtg acc atc aat aga atg atg agc		576
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser		
180	185	190
195		
<210> 36		
<211> 197		
<212> PRT		
<213> Felis catus		
<400> 36		
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu		
1	5	10
		15
Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys		
20	25	30
Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp		
35	40	45
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu		
50	55	60
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile		
65	70	75
		80
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe		
85	90	95

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr  
100 105 110

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu  
130 135 140

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser  
145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser  
180 185 190

Tyr Leu Asn Ala Ser  
195

<210> 37  
<211> 591  
<212> DNA  
<213> Felis catus

<400> 37  
ggaaggcattc agatagctca tcattctatt gatggtaact gcacgaattc tgaaagcatg 60  
aagaagtatg cagagcttga ttttagttt ataaaaatcc gggttcttcca aggaggagtt 120  
ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180  
catgtttga tccagaaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240  
cttgaactcc acctggtaaca tcttcaagtc ctcatacgata ctgctaaggc acagggtcgt 300  
cataaaagag gtctttctgg aggccaggca actcccattt aatccatggag agatctct 360  
ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct 420  
ggttttatct tttgtgatat cttcatgatc aatctttcg gaagtgcagg agtaaaattc 480  
tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgccaggcagg tttgggagtg 540  
gttggggcac tggAACATTC ctgggcttgg tgtgggtgtg gggaggttcc t 591

<210> 38  
<211> 1599

<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
<222> (1)..(1599)

<400> 38

atg cat cct cag cag ttg gtc atc gcc tgg ctt tcc ctg gtt ttg ctg	48
Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu	
1 5 10 15	
gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt	96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val	
20 25 30	
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc	144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag	192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln	
50 55 60	
agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa	240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65 70 75 80	
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt	288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val	
85 90 95	
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg	336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp	
100 105 110	
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt	384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe	
115 120 125	
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg	432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	
130 135 140	
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga	480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg	
145 150 155 160	
ggc tcc tct gac ccc caa gag gtg act tgt gga gca gcg aca ctc tca	528
Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser	
165 170 175	
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg	576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val	
180 185 190	

gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro 195 200 205	624
att gaa gtc gtg gtc gac gct att cac aag ctc aag tac gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210 215 220	672
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys 225 230 235 240	720
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245 250 255	768
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260 265 270	816
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275 280 285	864
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290 295 300	912
gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305 310 315 320	960
agc aac tgg gca tcc gtg tcc tgc agt ggt ggc ggt ggc ggc gga tct Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Ser 325 330 335	1008
aga aac ttg cca acc cct act cca tcc ccg ggg atg ttc cag tgc ctc Arg Asn Leu Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu 340 345 350	1056
aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys 355 360 365	1104
gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp 370 375 380	1152
cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu 385 390 395 400	1200
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile 405 410 415	1248
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt	1296

```
<210> 39
<211> 533
<212> PRT
<213> Felis catus

<400> 39
```

Met	His	Pro	Gln	Gln	Leu	Val	Ile	Ala	Trp	Leu	Ser	Leu	Val	Leu	Leu
1				5					10					15	

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val  
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln  
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val  
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg  
145 150 155 160

Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser  
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro  
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Ser  
325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu  
340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys  
355 360 365

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp  
370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu  
385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile  
405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe  
420 425 430

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr  
435 440 445

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu  
465 470 475 480

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser  
485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser  
515 520 525

Tyr Leu Asn Ala Ser  
530

<210> 40  
<211> 1599  
<212> DNA  
<213> Felis catus

<400> 40  
ggaagcattc agatagctca tcattctatt gatggtaact gcacgaattc tgaaagcatg 60  
aagaagtatg cagagcttga ttttagttt ataaaaatcc gggtttcca aggaggagtt 120  
ctgtggcaca gtcacactgt tgacatttag ggcctgtaac agctcatcaa tagctgtcag 180  
catgtttga tccagaaaaga tctgcctttt aggttccatt aacagctttg cattcatggc 240  
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300  
cataaaagag gtcttctgg aggccaggca actcccatta gttatcagag agatctct 360  
ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct 420  
ggtttatct tttgtgatat cttcatgatc aatctttcg gaagtgcagg agtaaaattc 480  
tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgccaggcagg tttgggagtg 540  
gttggggcac tggAACATCC ccggggatgg agtaggggtt ggcaagttc tagatccg 600  
gccaccgcca ccactgcagg acacggatgc ccagttgctc caggatgagc tatagtagcg 660  
gtctctggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720  
gtccacggag agtctgtctt tctttctct gttgttcttgc ccctggaccc gtacgcca 780  
tgttaaggag aagtaggaat gtggggtgct ccaggtgtca gggattccc agtcacttc 840  
cacatgccga gaattttta atggcttcag ttgcaggttc ttgggtgggt ccggtttgat 900  
gatgtccctg atgaagaagc tgctgggtgtac gtttcgtac ttgagcttgc gaatagcg 960  
caccacgact tcaatggta ggctctcctc ggcagccggg caggactgc ctcctgaca 1020  
ctccactgt tacttcttat aatccctgtt gtccactctg accttctctg ctgagagtgt 1080  
cgctgctcca caagtcacct ctgggggtc agaggagcct ctgctgctt tgacagtga 1140  
tttcaaatcg gtactgattt ccgtcagcca ccagcagggtg aaacgtccag aataattctt 1200  
tgcctcacat tttagaaaaga tcttattttt ggatttttc tgccctta agatatcgt 1260  
ggaccaaatt ccatcttcct tttgtgtat caggaggaac gaatggctca gaacctcg 1320  
tcctttatga caggtatact ggccagcatc tgcaaattct ttgacttggta tggtcagagt 1380  
tttaccagag cctaggactt cactgctctg gtcagaggc caggtgatgt catcttctc 1440

aggagtattg caggtgagga ccaccatttc tccggggca tcagggtgcc agtccaactc	1500
tacaacataa acgttttct ccagttccc tatggccatg aggggaggtg ccagcaaaac	1560
cagggaaagc caggcgatga ccaactgctg aggatgcat	1599

<210> 41  
<211> 576  
<212> DNA  
<213> *Felis catus*

<400> 41	
aattcttgtt ttgaacagtg aacattatgg acttatcccc attttcatcc tttttttca	60
aaatgagttt gaaaagatct ttctttttt cacaagctag aaagtacccc ttgtacaatg	120
aagactcaaa ttgtatctta tcatcatgtc ctggaacact tctctgaaag aatatgatgt	180
catttccttc atcattgata ctctcaggag gactcatttc cttaaaggaa ataattttgt	240
tctcacagga gagagttagac atggcttat aattcacaga gatggttact gccagacctc	300
tagtgaggct atcttatac atatatatga taaattcagt ccggggtgca ttatctgtac	360
agtcagaatc aggcatatcc tcaaacacag gttgatctcc ctggtaatg aagagaactt	420
ggtcgttcaa gtttcgtaag attgagagtt tatgttcaag ctgc当地aaag taatctgttt	480
ccaggttttc atcaactgtca gctacaaagt aaagtgtatt gtcaataaaat ttcattccca	540
caaagttgat gcaatcatct actggtagat cagtca	576

<210> 42  
<211> 0  
<212> DNA  
<213> *Felis catus*

<400> 42  
000

<210> 43  
<211> 1533  
<212> DNA  
<213> *Felis catus*

<220>  
<221> CDS  
<222> (1)..(1533)

<400> 43	
ata tgg gaa ctg gag aaa aac gtt tat gtt gta gag ttg gac tgg cac	48
Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His	
1 5 10 15	

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa		96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu		
20	25	30
 gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc		144
Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly		
35	40	45
 tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc		192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly		
50	55	60
 cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc		240
Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu		
65	70	80
 ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg		288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg		
85	90	95
 gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag		336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys		
100	105	110
 aat tat tct gga cgt ttc acc tgc tgg ctg acg gca atc agt acc		384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr		
115	120	125
 gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa		432
Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln		
130	135	140
 gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg		480
Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val		
145	150	155
160		
 gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt		528
Asp Asn Arg Asp Tyr Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser		
165	170	175
 gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac		576
Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp		
180	185	190
 gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc		624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile		
195	200	205
 agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca		672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro		
210	215	220
 tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc		720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr		
225	230	235
240		

tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val 245 250 255	768
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys 260 265 270	816
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln 275 280 285	864
gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg Ala Arg Asp Arg Tyr Tyr Ser Ser Trp Ser Asn Trp Ala Ser Val 290 295 300	912
tcc tgc agt ggt ggc ggt ggc ggc gga tct aga aac ttg cca acc cct Ser Cys Ser Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro 305 310 315 320	960
act cca tcc ccg ggg atg ttc cag tgc ctc aac cac tcc caa acc ctg Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu 325 330 335	1008
ctg cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu 340 345 350	1056
ttt tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys 355 360 365	1104
gat aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met 370 375 380	1152
aat gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly 385 390 395 400	1200
agt tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu 405 410 415	1248
agc agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala 420 425 430	1296
atg aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp 435 440 445	1344
caa aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val 450 455 460	1392
aac agt gtg act gtg cca cag aac tcc tcc ttg gaa gaa ccg gat ttt	1440

Asn Ser Val Thr Val Pro Gln Asn Ser Ser	Leu Glu Glu Pro Asp Phe			
465	470	475	480	
tat aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att				1488
Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu His Ala Phe Arg Ile				
485	490	495		
cgt gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc				1533
Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser				
500	505	510		
<210> 44				
<211> 511				
<212> PRT				
<213> Felis catus				
<400> 44				
Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His				
1	5	10	15	
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu				
20	25	30		
Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly				
35	40	45		
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly				
50	55	60		
Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu				
65	70	75	80	
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg				
85	90	95		
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys				
100	105	110		
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr				
115	120	125		
Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln				
130	135	140		
Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val				
145	150	155	160	

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser  
165 170 175

Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp  
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile  
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro  
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr  
225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val  
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys  
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln  
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val  
290 295 300

Ser Cys Ser Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro  
305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu  
325 330 335

Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu  
340 345 350

Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys  
355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met  
370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly  
385 390 395 400

Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu  
405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala  
420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp  
435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val  
450 455 460

Asn Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe  
465 470 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile  
485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser  
500 505 510

<210> 45  
<211> 1533  
<212> DNA  
<213> Felis catus

<400> 45  
ggaaggattc agatagctca tcattctatt gatggtaact gcacgaattc tgaaagcatg 60  
aagaagtatg cagagttga ttttagttt ataaaaatcc gggtttcca aggaggagtt 120  
ctgtggcaca gtcacactgt tgacatttag ggcctgtaac agtcatacaa tagtgcag 180  
catgtttga tccagaaaaga tctgcctttt aggttccatt aacagtttg cattcatggc 240  
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcg 300  
cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctct 360  
ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct 420  
gtttttatct tttgtgatat ctcatgatc aatctttcg gaagtgcagg agtaaaattc 480  
tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgccaggcagg tttgggagtg 540

gttggggcac	tggaacatcc	ccggggatgg	agttaggggtt	ggcaagtttc	tagatccgcc	600
gccaccgcca	ccactgcagg	acacggatgc	ccagttgctc	caggatgagc	tatagtagcg	660
gtctctggct	tgcacgcgga	tcttggcatc	cttgtggcac	acgaccttgg	ctgaggtctt	720
gtccacggag	agtctgtctt	tctttctct	gttgttcttg	ccctggacct	gtacgccaaa	780
tgttaaggag	aagtaggaat	gtggggtgct	ccaggtgtca	gggtattccc	agctcacttc	840
cacatgccga	gaattttta	atggcttcag	ttgcaggttc	ttgggtgggt	ccggtttgat	900
gatgtccctg	atgaagaagc	tgctggtgta	gtttcgtac	ttgagcttgc	aatagcgtc	960
caccacgact	tcaatgggta	ggctctcctc	ggcagccggg	caggcactgc	cctcctgaca	1020
ctccactgtg	tacttcttat	aatccctgtt	gtccactctg	accttctctg	ctgagagtgt	1080
cgctgctcca	caagtacact	ctgggggtc	agaggagcct	ctgctgcttt	tgacagtgaa	1140
tttcaaatacg	gtactgattt	ccgtcagcca	ccagcaggtg	aaacgtccag	aataattctt	1200
tgccctcacat	tttagaaaaga	tcttattttt	ggattcttc	tgttccctta	agatatcagt	1260
ggaccaaatt	ccatcttcct	ttttgtgtat	caggaggaac	gaatggctca	gaacctcgcc	1320
tcctttatga	caggtatact	ggccagcatc	tgcaaattct	ttgacttgaa	tggtcagagt	1380
tttaccagag	cctaggactt	cactgctctg	gtcagaggc	caggtgatgt	catcttcttc	1440
aggagtattt	caggtgagga	ccaccatttc	tccggggca	tcagggtgcc	agtccaaactc	1500
tacaacataa	acgaaaaat	ccagttcccc	tat			1533

<210> 46  
 <211> 666  
 <212> DNA  
 <213> Canis familiaris

<220>	
<221>	CDS
<222>	(1)..(666)
<400>	46
atg tgc ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta	48
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu	
1 5 10 15	
agc cac ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca	96
Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser	
20 25 30	
ccg agc cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg	144
Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu	
35 40 45	

aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta		192
Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu		
50	55	60
tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat		240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp		
65	70	75
aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat		288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn		
85	90	95
gag agt tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt		336
Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser		
100	105	110
tgc ctg gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc		384
Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser		
115	120	125
agc atc tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg		432
Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met		
130	135	140
aac gca aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa		480
Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln		
145	150	155
160		
aac atg ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac		528
Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn		
165	170	175
agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat		576
Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr		
180	185	190
aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt		624
Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg		
195	200	205
gcg gtg acc atc gat aga atg atg agt tat ctg aat tct tcc		666
Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser		
210	215	220

<210> 47  
<211> 222  
<212> PRT  
<213> Canis familiaris  
  
<400> 47

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu  
1               5                           10                           15

Ser	His	Leu	Asp	His	Leu	Thr	Trp	Ala	Arg	Ser	Leu	Pro	Thr	Ala	Ser
		20				25						30			
Pro	Ser	Pro	Gly	Ile	Phe	Gln	Cys	Leu	Asn	His	Ser	Gln	Asn	Leu	Leu
		35				40						45			
Arg	Ala	Val	Ser	Asn	Thr	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Leu
		50				55						60			
Tyr	Ser	Cys	Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp
		65			70			75				80			
Lys	Thr	Ser	Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Thr	Met	Asn
				85				90					95		
Glu	Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser
			100				105					110			
Cys	Leu	Ala	Ser	Gly	Lys	Ala	Ser	Phe	Met	Thr	Val	Leu	Cys	Leu	Ser
		115				120					125				
Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	Gln	Met	Glu	Phe	Lys	Ala	Met
		130				135				140					
Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln
		145				150				155			160		
Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu	Leu	Gln	Ala	Leu	Asn	Phe	Asn
		165				170					175				
Ser	Val	Thr	Val	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr
			180				185					190			
Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg
		195				200					205				
Ala	Val	Thr	Ile	Asp	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ser	Ser		
		210				215					220				
<210>	48														
<211>	666														
<212>	DNA														
<213>	Canis familiaris														

<400> 48  
 ggaagaattc agataactca tcattctatc gatggtcacc gcacgaattc tgaaagcatg 60  
 aagaagtatg cagagcttga ttttagttt ataaaaatcc ggctttcaa gggaggattt 120  
 ctgtggcaca gtcacactgt taaaattcag ggcctgtaac agctcatcga tagctgtcag 180  
 catgtttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240  
 cttgaattcc atctggtaca tcttcaagtc ctcatacatg ctgctaaggc acaggaccgt 300  
 cataaaagag gcctttccag aggccaggca actccgtta gttatcaaag agatctct 360  
 ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct 420  
 ggttttatcc tttgtgatat ctcatgatc aatctttcg gaagtgcagg aatataattc 480  
 tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcagcaggt tttggagtg 540  
 gttgaggcac tggaatattc ctgggctcgg tgaggctgtg gggaggctcc tggcccaagt 600  
 aaggtggtcc aggtggctta gcaggaccag gatggtcaca aggaggaggc cgcgccggcgg 660  
 gcacat 666

<210> 49  
 <211> 591  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)...(591)

<400> 49  
 agg agc ctc ccc aca gcc tca ccg agc cca gga ata ttc cag tgc ctc 48  
 Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu  
 1 5 10 15

aac cac tcc caa aac ctg ctg aga gcc gtc agc aac acg ctt cag aag 96  
 Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys  
 20 25 30

gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat 144  
 Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp  
 35 40 45

cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta 192  
 His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu  
 50 55 60

cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc 240  
 Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile  
 65 70 75 80

tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe 85 90 95	288
atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr 100 105 110	336
cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys 115 120 125	384
agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu 130 135 140	432
tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser 145 150 155 160	480
ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu 165 170 175	528
ctt cat gct ttc aga att cgt gcg gtg acc atc gat aga atg atg agt Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Met Met Ser 180 185 190	576
tat ctg aat tct tcc Tyr Leu Asn Ser Ser 195	591
<210> 50	
<211> 197	
<212> PRT	
<213> Canis familiaris	
<400> 50	
Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu 1 5 10 15	
Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys 20 25 30	
Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp 35 40 45	
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu 50 55 60	
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	

65

70

75

80

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe  
85 90 95

Met	Thr	Val	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr
			100					105					110		

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
           115               120               125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu  
130 135 140

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser  
145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Met Met Ser  
180 185 190

Tyr Leu Asn Ser Ser  
195

<210> 51  
<211> 591  
<212> DNA  
<213> *Canis familiaris*

```
<400> 51
ggaagaattc agataactca tcatttatac gatggtcacc gcacgaattc taaaaggcatg      60
aagaagtatg cagagcttga ttttagttt ataaaaatcc ggcttcaa gggaggattt      120
ctgtggcaca gtcacactgt taaaattcag ggcctgtaac agctcatcga tagctgtcag      180
catgtttga tccagaaaaga tctgcctttt gggatccatt aaaagctttg cgttcatggc      240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt      300
cataaaagag gccttccag aggccaggca actcccgtt aatcaaaag agatctctct      360
ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct      420
ggttttatcc tttgtatcat cttcatgatc aatctttcg gaagtgcagg aatataattc      480
```

tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcagcaggt tttgggagtg	540
gttgaggcac tggaatattc ctgggctcggtgaggctgtggaggctcc t	591
<210> 52	
<211> 921	
<212> DNA	
<213> Canis familiaris	
<220>	
<221> CDS	
<222> (1)..(921)	
<400> 52	
ata tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac	48
Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His	
1                         5                         10                         15	
cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa	96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu	
20                         25                         30	
gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt	144
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly	
35                         40                         45	
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc	192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly	
50                         55                         60	
cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg	240
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu	
65                         70                         75                         80	
ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag	288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys	
85                         90                         95	
gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag	336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys	
100                         105                         110	
aat tat tct gga cgt ttc aca tgc tgg ctg acg gca atc agt act	384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr	
115                         120                         125	
gat ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa	432
Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln	
130                         135                         140	
ggg gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg	480
Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val	
145                         150                         155                         160	
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt	528

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser			
165	170	175	
gcc tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat			576
Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp			
180	185	190	
gct att cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc			624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile			
195	200	205	
aga gac atc atc aaa cca gac cca ccc aca aac ctg cag ctg aag cca			672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro			
210	215	220	
ttg aaa aat tct cgg cac gtg gag gtc agc tgg gaa tac ccc gac acc			720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr			
225	230	235	240
tgg agc acc cca cat tcc tac ttc tcc ctg aca ttt tgc ata cag gcc			768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala			
245	250	255	
cag ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag			816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys			
260	265	270	
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa			864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln			
275	280	285	
gcc cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg			912
Ala Arg Asp Arg Tyr Tyr Ser Ser Trp Ser Asp Trp Ala Ser Val			
290	295	300	
tcc tgc agt			921
Ser Cys Ser			
305			
<210> 53			
<211> 307			
<212> PRT			
<213> Canis familiaris			
<400> 53			
Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His			
1	5	10	15
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu			
20	25	30	
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly			
35	40	45	

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly  
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu  
65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys  
85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys  
100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr  
115 120 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln  
130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val  
145 150 155 160

Asp Asn Arg Asp Tyr Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser  
165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp  
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile  
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro  
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr  
225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala  
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys  
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln  
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val  
290 295 300

Ser Cys Ser  
305

```
<210> 54
<211> 921
<212> DNA
<213> Canis familiaris
```

<400> 54  
actgcaggac acagatgccc agtcgctcca ggatgaacta tagtagcggt ctcgggcttg 60  
cacgcggatc ttggcatcct tgtggcacac gaccttgct gaggtcttgt ccacgcagag 120  
tctatcttc ttttctctat tgttcttgcc ctgggcctgt atgcaaaatg tcagggagaa 180  
gtaggaatgt ggggtgctcc aggtgtcggg gtattccag ctgacctcca cgtgccgaga 240  
attttcaat ggcttcagct gcaggtttgt gggtggtct ggtttgatga tgtctctgat 300  
gaagaagctg ctggtgttagt tttcatactt gagcttgta atagcatcca ccacgaccc 360  
gatgggttagg ctctcctcgg cagagggca ggcactgccc tcctgacact ccactgtgta 420  
cttcttataa tccctgttgt ccactctgac cctctctgct gaaagtgtca ctgctccaca 480  
tgtcacccct tgggggtcag agaaggctct gctactttg acactgaatt tcaaatacg 540  
actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattcttg cctcacattt 600  
cagaaagatc ttatTTTgg attcttctg tccctttaag atatcagtgg accaaattcc 660  
atcttcttt ttgtgaatca acaggagtga gcggctcaga accttgccctc ctttatggca 720  
ggtatactgg ccagcatctc caaatcttt gacttggatg gtcagagttt taccagaacc 780  
taggacttca ctgctctgcg ctgagggtcca agtgatgtca tcttcttcag gggtatggca 840  
ggtgaggacc accatttctc cggggcatac agggtgccag tccaactcta caacataaac 900  
atctttctcc agttccccata t 921

```
<210> 55
<211> 985
<212> DNA
<213> Felis catus
```

<220>  
 <221> CDS  
 <222> (1)...(984)

<400>	55		
atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg			48
Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu			
1	5	10	15
gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt			96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val			
20	25	30	
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc			144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu			
35	40	45	
acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag			192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln			
50	55	60	
agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa			240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys			
65	70	75	80
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt			288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val			
85	90	95	
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg			336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp			
100	105	110	
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt			384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe			
115	120	125	
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg			432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp			
130	135	140	
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga			480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg			
145	150	155	160
ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca			528
Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser			
165	170	175	
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg			576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val			
180	185	190	
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc			624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro			
195	200	205	

att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210	215	220	672
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys 225	230	235	720
aac ctg caa ctg aag cca tta aaa aat tct cggttcatgtgaaatgtgagc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245	250	255	768
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260	265	270	816
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275	280	285	864
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290	295	300	912
gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305	310	315	960
agc aac tgg gca tcc gtg tcc tgc a Ser Asn Trp Ala Ser Val Ser Cys 325			985

<210>	56
<211>	328
<212>	PRT
<213>	Felis catus

<400> 56

Met	His	Pro	Gln	Gln	Leu	Val	Ile	Ala	Trp	Phe	Ser	Leu	Val	Leu	Leu
1				5					10					15	

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val  
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln  
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val  
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg  
145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser  
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro  
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

290

295

300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
 305                    310                    315                    320

Ser Asn Trp Ala Ser Val Ser Cys  
325

<210> 57  
<211> 985  
<212> DNA  
<213> *Felis catus*

<400> 57  
tgcaggacac ggatgccag ttgctccagg atgagctata gtagcggtct ctggcttgca 60  
cgcggatctt ggcatttcgt tggcacacga cttggctga ggtttgtcc acggagagtc 120  
tgtctttctt ttctctgttg ttcttgcctt ggacctgtac gccaaatgtt aaggagaagt 180  
aggaatgtgg ggtgctccag gtgtcagggt attcccagct cactccaca tgccgagaat 240  
tttttaatgg cttagttgc aggttcttgg gtgggtccgg tttgatgtatg tccctgtatga 300  
agaagctgct ggtgttagtt tcgtacttga gcttgtgaat agcgtccacc acgacttcaa 360  
tgggtaggct ctccctcgca gccgggcagg cactgcctc ctgacactcc actgtgtact 420  
tcttataatc cctgttgc actctgaccc tctctgtga gagtgcgtct gctccacaag 480  
tcaccccttg ggggtcagag gagcctctgc tgctttgac agtgaatttc aaatcggtac 540  
tgattgccgt cagccaccag caggtgaaac gtccagaata attcttgcc tcacattta 600  
gaaagatctt attttggat tctttctgtt cccttaagat atcagtggac caaattccat 660  
cttcctttt gtgtatcagg aggaacgaat ggctcagaac ctcgcctcct ttatgacagg 720  
tatactggcc agcatctgca aattcttga cttggatggt cagagttta ccagagccta 780  
ggacttcact gctctggta gaggtccagg ttagtgcata ttcttcagga gtattgcagg 840  
tgaggaccac catttctccg ggggcatcag ggtgccagtc caactctaca acataaacgt 900  
ttttctccag ttccccatatg gccatgaggg gaggtgccag caaaaaccagg gaaaaaccagg 960  
cgatgaccaa ctgctgagga tgcac 985

<210> 58  
<211> 987  
<212> DNA  
<213> *Canis familiaris*

<220>  
 <221> CDS  
 <222> (1)...(987)

<400>	58		
atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctc gtt ttg ctg		48	
Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu			
1	5	10	15
gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt		96	
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val			
20	25	30	
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc		144	
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu			
35	40	45	
acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag		192	
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln			
50	55	60	
agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa		240	
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys			
65	70	75	80
gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt		288	
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val			
85	90	95	
ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg		336	
Leu Ser Arg Ser Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp			
100	105	110	
tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt		384	
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe			
115	120	125	
ctg aaa tgt gag gca aag aat tat tct gga cgt ttc aca tgc tgg tgg		432	
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp			
130	135	140	
ctg acg gca atc agt act gat ttg aaa ttc agt gtc aaa agt agc aga		480	
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg			
145	150	155	160
ggc ttc tct gac ccc caa ggg gtg aca tgt gga gca gtg aca ctt tca		528	
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser			
165	170	175	
gca gag agg gtc aga gtg gac aac agg gat tat aag aag tac aca gtg		576	
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val			
180	185	190	
gag tgt cag gag ggc agt gcc tgc ccc tct gcc gag gag agc cta ccc		624	
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro			
195	200	205	

atc gag gtc gtg gtg gat gct att cac aag ctc aag tat gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210	215	220	672
acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca Thr Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr 225	230	235	720
aac ctg cag ctg aag cca ttg aaa aat tct cggttgg cac gtg gag gtc agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245	250	255	768
tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260	265	270	816
aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275	280	285	864
aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290	295	300	912
gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305	310	315	960
agc gac tgg gca tct gtg tca tgc agt Ser Asp Trp Ala Ser Val Ser Cys Ser 325			987

<210> 59  
<211> 329  
<212> PRT  
<213> Canis familiaris

<400> 59

Met	His	Pro	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Leu	Leu
1				5					10					15	

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val  
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln  
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val  
85 90 95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg  
145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser  
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro  
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

290

295

300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser  
325

<210> 60  
<211> 987  
<212> DNA  
<213> Canis familiaris

<400> 60  
actgcatgac acagatgccc agtcgctcca gnatgaacta tagtagcggt ctcgggcttg 60  
cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtcttgt ccacgcagag 120  
tctatctttc ttttctctat ttttcttgcc ctgggcctgt atgcaaaatg tcagggagaa 180  
gttaggaatgt ggggtgctcc aggtgtcggt gtattccag ctgaccccca cgtgccgaga 240  
attttcaat ggcttcagct gcagggttgtt ggggtgggtct ggtttgcata tgtctctgat 300  
gaagaagctg ctgggttagt tttcatactt gagcttgcata atagcatccca ccacgacactc 360  
gatgggttagg ctctccctcg cagagggca ggcactgccc tcctgacact ccactgtgta 420  
cttcttataa tccctgttgtt ccactctgac cctctctgct gaaagtgtca ctgctccaca 480  
tgtcacccct tgggggtcag agaagcctct gctacttttgc acactgaatt tcaaatacgat 540  
actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattcttgc cctcacattt 600  
cagaaagatc ttatTTTGG attcttctg ttcctttaag atatcagtgg accaaattcc 660  
atcttctttt ttgtgaatca acaggagtga gcggctcaga accttgcctc ctttatggca 720  
ggtatactgg ccagcatctc caaattctt gacttggatg gtcagatgtt taccagaacc 780  
taggacttca ctgctctgctg ctgaggtcca agtgcgtca tcttcttgc gggatggca 840  
ggtgaggacc accattctc cggggccatc aggggtgccag tccaaactcta caacataaac 900  
atcttctcc agttccata tggccatgag gggagacgcc agcaaaacga gggaaaacca 960  
ggagatgacc aactgctgag ggtgcatt 987

<210> 61  
<211> 1599  
<212> DNA  
<213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)...(1599)

<400>	61			
atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctc gtt ttg ctg				48
Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu				
1	5	10	15	
gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt				96
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val				
20	25	30		
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc				144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu				
35	40	45		
acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag				192
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln				
50	55	60		
agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa				240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys				
65	70	75	80	
gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt				288
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val				
85	90	95		
ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg				336
Leu Ser Arg Ser Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp				
100	105	110		
tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt				384
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe				
115	120	125		
ctg aaa tgt gag gca aag aat tat tct gga cgt ttc aca tgc tgg tgg				432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp				
130	135	140		
ctg acg gca atc agt act gat ttg aaa ttc agt gtc aaa agt agc aga				480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg				
145	150	155	160	
ggc ttc tct gac ccc caa ggg gtg aca tgt gga gca gtg aca ctt tca				528
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser				
165	170	175		
gca gag agg gtc aga gtg gac aac agg gat tat aag aag tac aca gtg				576
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val				
180	185	190		
gag tgt cag gag ggc agt gcc tgc ccc tct gcc gag gag agc cta ccc				624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro				
195	200	205		

atc gag gtc gtg gat gct att cac aag ctc aag tat gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	672
210 215 220	
acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr	720
225 230 235 240	
aac ctg cag ctg aag cca ttg aaa aat tct cggt cac gtg gag gtc agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser	768
245 250 255	
tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu	816
260 265 270	
aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	864
275 280 285	
aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	912
290 295 300	
gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp	960
305 310 315 320	
agc gac tgg gca tct gtg tca tgc agt ggt ggc ggt ggc gga tct Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Ser	1008
325 330 335	
aga aac ttg cca acc cct act cca tcc ccg ggt atg ttccaa tgt ttg Arg Asn Leu Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu	1056
340 345 350	
aac cac tcc caa acc ttg ttg aga gcc gtc agc aac acg ctt cag aag Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys	1104
355 360 365	
gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp	1152
370 375 380	
cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	1200
385 390 395 400	
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	1248
405 410 415	
tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe	1296
420 425 430	

atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac		1344	
Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr			
435	440	445	
cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag		1392	
Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys			
450	455	460	
agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg		1440	
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu			
465	470	475	480
tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc		1488	
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser			
485	490	495	
ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt		1536	
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu			
500	505	510	
ctt cat gct ttc aga att cgt gcg gtg acc atc aat aga atg atg tcc		1584	
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser			
515	520	525	
tac ttg aac tct tcc		1599	
Tyr Leu Asn Ser Ser			
530			

<210> 62  
<211> 533  
<212> PRT  
<213> Canis familiaris

<400> 62

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu  
1 5 10 15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val  
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln  
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val

85

90

95

Leu Ser Arg Ser Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg  
145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser  
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro  
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Ser  
325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu  
340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys  
355 360 365

Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp  
370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu  
385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile  
405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe  
420 425 430

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr  
435 440 445

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu  
465 470 475 480

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser  
485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser  
515 520 525

Tyr Leu Asn Ser Ser  
530

<210> 63  
 <211> 1599  
 <212> DNA  
 <213> Canis familiaris

<400> 63	
ggaagagttc aagttaggaca tcattctatt gatggtcacc gcacgaattc tgaaagcatg	60
aagaagtatg cagagcttga ttttagttt ataaaaatcc ggctttcaa gggaggattt	120
ctgtggcaca gtcacactgt tgaaatttag ggcctgtaac agctcatcga tagctgtcag	180
catgtttga tccagaaaaga tctgcctttt gggatccatt aaaagctttg cgttcatggc	240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt	300
cataaaagag gcctttccag aggccaggca actcccgtaa gttatcaaag agatctct	360
ggaagccagg caactctcat tcatggtaa ttccagtgg aagcaggcct ccactgtgct	420
ggtttatcc tttgtgatat ctcatgatc aatctttcg gaagtgcagg aatataattc	480
tagagttgt ctggcccttctt gaagcgtgtt gctgacggct ctcaacaagg tttgggagtg	540
gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc	600
gccaccggcca ccactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg	660
gtctcgggct tgcacgcga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt	720
gtccacgcag agtctatctt tctttctctt attgttcttgc ccctgggcct gtatgcaaaa	780
tgtcagggag aagtaggaat gtggggtgct ccaggtgtcg gggattccc agctgacctc	840
cacgtgccga gaattttca atggcttcag ctgcaggaaa gtgggtgggt ctgggttgc	900
gatgtctctg atgaagaagc tgctggtgta gtttcatac ttgagcttgt gaatagcatc	960
caccacgacc tcgatggta ggctctcctc ggcagagggg caggcactgc ctcctgaca	1020
ctccactgtg tacttcttat aatccctgtt gtccactctg accctctctg ctgaaagtgt	1080
cactgctcca catgtcaccc ctgggggtc agagaagcct ctgctacttt tgacactgaa	1140
tttcaaatac gtactgattt ccgtcagccca ccagcatgtg aaacgtccag aataatttt	1200
tgcctcacat ttcaaaaaa tcttattttt ggatttttc tgttccttta agatatcgt	1260
ggaccaaattt ccatcttctt ttttgtgaat caacaggagt gagcggctca gaaccttgcc	1320
tcctttaggg caggtataact ggcagcatc tccaaattct ttgacttgaa tggcagagt	1380
tttaccagaa cctaggactt cactgctctg cgctgaggc caagtgtatgt catcttcttc	1440
agggtatgg caggtgagga ccaccatttc tccggggca tcagggtgcc agtccaactc	1500

tacaacataa acatcttct ccagttccca tatggccatg aggggagacg ccagcaaaac	1560
gagggaaaac caggagatga ccaactgctg agggtgcat	1599
<210> 64	
<211> 0	
<212> DNA	
<213> Canis familiaris	
<400> 64	
000	
<210> 65	
<211> 0	
<212> DNA	
<213> Canis familiaris	
<400> 65	
000	
<210> 66	
<211> 1533	
<212> DNA	
<213> Canis familiaris	
<220>	
<221> CDS	
<222> (1)..(1533)	
<400> 66	
ata tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac	48
Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His	
1                         5                         10                         15	
cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa	96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu	
20                         25                         30	
gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt	144
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly	
35                         40                         45	
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc	192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly	
50                         55                         60	
cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgcc tca ctc ctg	240
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu	
65                         70                         75                         80	
ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag	288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys	
85                         90                         95	
gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag	336

Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys	
100																110
aat	tat	tct	gga	cgt	ttc	aca	tgc	tgg	tgg	ctg	acg	gca	atc	agt	act	384
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr	
115																125
gat	ttg	aaa	ttc	agt	gtc	aaa	agt	agc	aga	ggc	ttc	tct	gac	ccc	caa	432
Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	Gly	Phe	Ser	Asp	Pro	Gln	
130																140
ggg	gtg	aca	tgt	gga	gca	gtg	aca	ctt	tca	gca	gag	agg	gtc	aga	gtg	480
Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	Ala	Glu	Arg	Val	Arg	Val	
145																155
gac	aac	agg	gat	tat	aag	aag	tac	aca	gtg	gag	tgt	cag	gag	ggc	agt	528
Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser	
165																175
gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	atc	gag	gtc	gtg	gtg	gat	576
Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp	
180																190
gct	att	cac	aag	ctc	aag	tat	gaa	aac	tac	acc	agc	agc	ttc	ttc	atc	624
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	
195																205
aga	gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	672
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro	
210																220
ttg	aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	720
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	
225																235
tgg	agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	768
Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala	
245																255
cag	ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	816
Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys	
260																270
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	864
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	
275																285
gcc	cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	912
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val	
290																300
tca	tgc	agt	ggt	ggc	ggc	ggc	gga	tct	aga	aac	ttg	cca	acc	cct		960
Ser	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Arg	Asn	Leu	Pro	Thr	Pro	
305																310
act	cca	tcc	ccg	ggt	atg	ttc	caa	tgt	ttg	aac	cac	tcc	caa	acc	ttg	1008
Thr	Pro	Ser	Pro	Gly	Met	Phe	Gln	Cys	Leu	Asn	His	Ser	Gln	Thr	Leu	

325	330	335	
ttg aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu 340	345	350	1056
tta tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys 355	360	365	1104
gat aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met 370	375	380	1152
aat gag agt tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly 385	390	395	1200
agt tgc ctg gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu 405	410	415	1248
agc agc atc tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala 420	425	430	1296
atg aac gca aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp 435	440	445	1344
caa aac atg ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe 450	455	460	1392
aac agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe 465	470	475	1440
tat aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile 485	490	495	1488
cgt gcg gtg acc atc aat aga atg atg tcc tac ttg aac tct tcc Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser 500	505	510	1533
<210> 67			
<211> 511			
<212> PRT			
<213> Canis familiaris			
<400> 67			
Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His			
1	5	10	15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu  
20 25 30

Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly  
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly  
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu  
65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys  
85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys  
100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr  
115 120 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln  
130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val  
145 150 155 160

Asp Asn Arg Asp Tyr Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser  
165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp  
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile  
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro  
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr  
225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala  
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys  
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln  
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val  
290 295 300

Ser Cys Ser Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro  
305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu  
325 330 335

Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu  
340 345 350

Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys  
355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met  
370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly  
385 390 395 400

Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu  
405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala  
420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp  
435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe  
450 455 460

Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe

465

470

475

480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile  
 485                   490                   495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser  
 500                   505                   510

<210> 68  
<211> 1533  
<212> DNA  
<213> Canis familiaris

<400> 68	
ggaagagttc aagttaggaca tcattctatt gatggtcacc gcacgaattc tgaaagcatg	60
aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctttcaa gggaggattt	120
ctgtggcaca gtcacactgt taaaattcag ggcctgtaac agctcatcga tagctgtcag	180
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc	240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt	300
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctct	360
ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct	420
ggtttatcc ttgtgatat cttcatgatc aatctttcg gaagtgcagg aatataattc	480
tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcaacaagg tttgggagtg	540
gttcaaacat tggAACATAC ccggggatgg agtaggggtt ggcaagtttc tagatccgcc	600
gccaccgcca ccactgcattt acacagatgc ccagtcgctc caggatgaac tatagtagcg	660
gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt	720
gtccacgcag agtctatctt tctttctctt attgttcttg ccctgggcct gtatgaaaa	780
tgtcagggag aagtaggaat gtggggtgct ccaggtgtcg gggatttccc agctgacctc	840
cacgtgccga gaattttca atggcttcag ctgcagggtt gtgggtgggt ctggtttgc	900
gatgtctctg atgaagaagc tgcgtgtta gtttcatac ttgagcttgt gaatagcatc	960
caccacgacc tcgatggta ggctctcctc ggcagagggg caggcactgc cctcctgaca	1020
ctccactgtg tacttcttat aatccctgtt gtccactctg accctctctg ctgaaagtgt	1080
cactgctcca catgtcaccc ctgggggtc agagaaggct ctgctacttt tgacactgaa	1140
tttcaaatca gtactgattt ccgtcagcca ccagcatgtg aaacgtccag aataattctt	1200

tgccctcacat ttcagaaaaga tcttattttt ggatttttc tgttcctta agatatcgt	1260
ggaccaaatt ccatcttctt ttttgtaat caacaggagt gagcggctca gaaccttgcc	1320
tcccttatgg caggtatact ggcagcatac tccaaattct ttgacttgga tggtcagagt	1380
tttaccagaa cctaggactt cactgctctg cgctgaggc caagtatgt catttcttc	1440
agggtatgg caggtgagga ccaccatttc tccggggca tcagggtgcc agtccaactc	1500
tacaacataa acatcttctt ccagttccca tat	1533

<210> 69	
<211> 30	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	
<400> 69	
gc当地agctcg aaattaaccc tcactaaagg	30

<210> 70	
<211> 28	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	
<400> 70	
cgacggccag tgaattgtaa tacgactc	28

<210> 71	
<211> 31	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	
<400> 71	
agtatgttggaaatc agattactttt g	31

<210> 72	
<211> 32	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	

<400> 72	
atgcctgga acacttctct gaaagaatat ga	32
<210> 73	
<211> 30	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	
<400> 73	
aactatttag cacaggata aagatgactg	30
<210> 74	
<211> 33	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	
<400> 74	
aatatctaat tcttgaaaa aacagtgaac att	33
<210> 75	
<211> 36	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	
<400> 75	
tatgccggct actttggcaa gcttgaacat aaactc	36
<210> 76	
<211> 37	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	
<400> 76	
ggcctcgagc taattcttgt tttgaacagt gaacatt	37
<210> 77	
<211> 28	
<212> DNA	
<213> Artificial sequence	

<220>		
<223> Synthetic Primer		
<400> 77		
atggccgaca aggtcctgaa ggagaaga	28	
<210> 78		
<211> 33		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 78		
ttaatgtcct gggaaagaggt agaaaacatct tgt	33	
<210> 79		
<211> 26		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 79		
tcaagccccac aatctggaaa ttctca	26	
<210> 80		
<211> 26		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 80		
ctggagagtc actgatcaac agttcc	26	
<210> 81		
<211> 36		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 81		
acaaggatcc accatggccg acaaggatct gaaggg	36	
<210> 82		
<211> 39		

<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 82		
cgcccttaga cctcaattgc cagggaaagag atagaagta		39
<210> 83		
<211> 60		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 83		
ctgcagtggc ggcgggtggcg gcggatctag aaacttgcca acccctactc catccccggg		60
<210> 84		
<211> 60		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 84		
cccggggatg gagtaggggt tggcaagttt ctagatccgc cgccaccgccc accactgcag		60
<210> 85		
<211> 28		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 85		
atgcatcctc agcagttggc catcgct		28
<210> 86		
<211> 25		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 86		
tgcaggacac ggatgcccag ttgct		25

<210> 87	
<211> 37	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	
<400> 87	
acaggtacca tgcattcctca gcagttggtc atcgctt	37
<210> 88	
<211> 25	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	
<400> 88	
ctaactgcag gacacggatg cccag	25
<210> 89	
<211> 19	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	
<400> 89	
atgtgccccgc cgcggtggcc	19
<210> 90	
<211> 27	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	
<400> 90	
cttaggaagca ttcatatgc tcatacat	27
<210> 91	
<211> 39	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic Primer	

<400> 91		
tatgacccgg ggatgttcca gtgcctcaac cactccaa		39
<210> 92		
<211> 41		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 92		
atgactgcgg ccgccttagga agcattcaga tagctcatca t		41
<210> 93		
<211> 20		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 93		
ccatcctggc cctgctaaggc		20
<210> 94		
<211> 22		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 94		
ccatctggta catcttcaag tc		22
<210> 95		
<211> 38		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 95		
aaaaaacccg ggtatgttcc aatgtttcaa ccactccc		38
<210> 96		
<211> 51		
<212> DNA		
<213> Artificial sequence		

<220>		
<223> Synthetic Primer		
<400> 96		
gcggccgctc gagttaggaa gagttcaagt aggacatcat tctattgatg g		51
<210> 97		
<211> 22		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 97		
cttaaaggaa cagaaagaat cc		22
<210> 98		
<211> 19		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 98		
ggtattccca gctgacctc		19
<210> 99		
<211> 37		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 99		
cataggtacc atgcaccctc agcagtttgtt catctcc		37
<210> 100		
<211> 29		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic Primer		
<400> 100		
atctaaatgc atgacacacaga tgcccagtc		29
<210> 101		
<211> 561		

<212> DNA  
<213> *Felis catus*

<220>  
<221> CDS  
<222> (1)..(561)

<400> 101

```

ggg atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg cga gcc atc      48
Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
1          5           10          15

```

```

agc aac acg ctt cag aag gcc aga caa act cta gaa ttt tac tcc tgc 96
Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys
          20           25           30

```

act tcc gaa gag att gat cat gaa gat atc aca aaa gat aaa acc agc 144  
 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser  
                  35                 40                 45

aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt tgc 192  
Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys  
50 55 60

ctg gct tcc aga gag atc tct ctg ata act aat ggg agt tgc ctg gcc 240  
 Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala  
 65 70 75 80

tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc agt atc tat	288	
Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr		
85	90	95

gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg aat gca aag 336  
 Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys  
     100                105                110

ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa aac atg ctg 384  
 Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu  
     115             120             125

```

aca gct att gag ctg tta cag gcc ctg aat gtc aac agt gtg act      432
Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr
          130           135           140

```

```

gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat aaa act aaa      480
Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
145           150                  155          160

```

atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gca gtg acc 528  
Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr  
165 170 175

atc aat aga atg atg agc tat ctg aat gct tcc 561  
Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser  
180 185

<210> 102  
<211> 187  
<212> PRT  
<213> Felis catus

<400> 102

Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile  
1 5 10 15

Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys  
20 25 30

Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser  
35 40 45

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys  
50 55 60

Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala  
65 70 75 80

Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr  
85 90 95

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys  
100 105 110

Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu  
115 120 125

Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr  
130 135 140

Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys  
145 150 155 160

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr  
165 170 175

Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser  
180 185

<210> 103

<211> 561  
<212> DNA  
<213> Felis catus

<400> 103  
ggaagcattc agatagctca tcattctatt gatggtaact gcacgaattc tgaaagcatg 60  
aagaagtatg cagagcttga ttttagttt ataaaaatcc ggttcttcca gggaggagtt 120  
ctgtggcaca gtcacactgt tgacatttag ggcctgtaac agctcatcaa tagctgtcag 180  
catgtttga tccagaaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240  
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300  
cataaaagag gtcttctgg aggccaggca actcccatta gttatcagag agatctct 360  
ggaagccagg caactctcat tcatggtaa ttccagtggt aagcaggcct ccactgtgct 420  
ggtttatct tttgtgatat ctcatgatc aatctttcg gaagtgcagg agtaaaattc 480  
tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgccaggcagg tttgggagtg 540  
gtttagggcac tggaaacatcc c 561

<210> 104  
<211> 1455  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (232)..(897)

<400> 104  
ggcacgaggc aaaccccgcg ggcccagctc cacgtgtcac cgagaagctg atgtagagag 60  
agacagagag agaaagcaag ccggacaccg gagtcccggg aaagtccctgg cgccgcctcg 120  
gccaattata aaaatgtgac cccccgggtc ggcctccac cgccgcctc ccctgcccgc 180  
tccgcagtcc gcgtccagcg cccgcccggg tccacgcagc gcccgcctc c atg tgc 237  
Met Cys  
1  
ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta agc cac 285  
Pro Pro Arg Gly Leu Leu Val Thr Ile Leu Val Leu Leu Ser His  
5 10 15  
ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca ccg agc 333  
Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser Pro Ser  
20 25 30  
cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg aga gcc 381  
Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu Arg Ala

35	40	45	50	
gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta tat tcc Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu Tyr Ser				429
55	60	65		
tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat aaa acc Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr				477
70	75	80		
agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser				525
85	90	95		
tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt tgc ctg Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu				573
100	105	110		
gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc agc atc Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser Ser Ile				621
115	120	125	130	
tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg aac gca Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met Asn Ala				669
135	140	145		
aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa aac atg Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met				717
150	155	160		
ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac agt gtg Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn Ser Val				765
165	170	175		
act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat aaa act Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr				813
180	185	190		
aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gcg gtg Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val				861
195	200	205	210	
acc atc gat aga atg atg agt tat ctg aat tct tcc taaaaagctg Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser				907
215	220			
aggctctctc cgactttaaa gtcattccta taaaaatgtg aacccaaaag aattttcat				967
aagatagggg ttaagaacca gggaggggggt ggcttgacct ggctctactt aagcttagtac				1027
gataattctc atgcttgttt acattagttg ccactcaa at tttgaaagat gtgactgtta				1087
tatccccacac gatgcctttg accaagtata tttcacattt actatggata agttaagtgt				1147
tcgtgagcaa attgctaaag aggaaaaatg tcctcaccga acatgtttt atttccctt				1207
taatagaaga gcaagacttt ataagctatt tctgtaccaa actgtttgta gaaacaaaca				1267

ctcaagcata atttatttaa aaatacttat ttatataatt ttgtgttcat gaaagcatgt 1327  
gaattaattt atatttatTT atgttatTT tattaaagta tttattatca agtggatttg 1387  
ggatatctta tgTTctaaaa ataaaatgtat tgagttagaa aaaaaaaaaa aaaaaaaaaa 1447  
aaaaaaaaa 1455

<210> 105  
<211> 222  
<212> PRT  
<213> Canis familiaris  
  
<400> 105

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu  
1 5 10 15

Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser  
20 25 30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu  
35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu  
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp  
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn  
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser  
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser  
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met  
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln  
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn  
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr  
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg  
195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser  
210 215 220

<210> 106  
<211> 1455  
<212> DNA  
<213> Canis familiaris

<400> 106  
ttttttttt tttttttttt tttttttttt tctactcaat cattttattt tttagaacata 60  
agatatccca aatccacttg ataataaaata cttaataaaa tataacataaa ataaatataa 120  
attaattcac atgcttcat gaacacaaaa ttatataaat aagtattttt aaataaatta 180  
tgcttgagtg tttgttctca caaacagttt ggtacagaaa tagcttataa agtcttgctc 240  
ttctattaaa gggaaaataa aaacatgttc ggtgaggaca ttttcctct ttagcaattt 300  
gctcacgaac acttaactta tccatagtaa atgtgaaata tacttggtca aaggcatcgt 360  
gtgggatata acagtcacat cttcaaaat ttgagtgca actaatgtaa acaagcatga 420  
gaattatcgt actagcttaa gtaggaccag gtcaagccac cccctccctg gttcttaacc 480  
cctatcttat gaaaaattct ttgggttca cattttata ggaatgactt taaagtcag 540  
agagacctca gcttttagg aagaattcag ataactcatc attctatcga tggtcaccgc 600  
acgaattctg aaagcatgaa gaagtatgca gagcttgatt ttagtttat aaaaatccgg 660  
ctcttcaagg gaggattct gtggcacagt cacactgtt aattcaggg cctgtaacag 720  
ctcatcgata gctgtcagca tgggttgc cagaaagatc tgccctttg gatccattaa 780  
aagctttcg ttcatggcct tgaattccat ctggtacatc ttcaagtccct catagatgct 840  
gctaaggcac aggaccgtca taaaagaggg cttccagag gccaggcaac tcccgtagt 900  
tatcaaagag atctctctgg aagccaggca actctcattt atggtaatt ccagtggtaa 960  
gcaggcctcc actgtgctgg tttatcctt tgtgatatct tcatgatcaa tctcttcgga 1020  
agtgcaggaa tataattcta gagttgtct ggccttctga agcgtgttgc tgacggctct 1080

cagcaggttt	tgggagtggt	tgaggcactg	gaatattcct	gggctcggtg	aggctgtggg	1140
gaggctcctg	gcccaagtaa	ggtggtccag	gtggcttagc	aggaccagga	tggtcacaag	1200
gaggaggccg	cgcggcgggc	acatgctggg	cgggcgtgc	gtggaccccgg	gcgggcgtg	1260
gacgcggact	gcggacgcgg	caggggaggg	cggcggtggt	aggccgaccc	gggggggtcac	1320
attttataa	ttggcccgag	gcgcgccagg	actttcccg	gactccggtg	tccggcttgc	1380
tttctctctc	tgtctctctc	tacatcagct	tctcggtgac	acgtggagct	gggcccgcgg	1440
ggtttgcctc	gtgcc					1455

<210> 107  
<211> 2267  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (154)..(1140)

<400> 107																
ggcacgaggc	aacttggaca	agtca	gtt	tagttaagt	ttccatccaa	aagctcggt	60									
ggagtagggt	atataagctc	cagtagcagt	agcagcagca	gcaggagact	ccgtt	caga	120									
cccagggaac	cttgcagcct	ggccaga	aag	atg	cat	cct	cag	cag	ttg	gtc	174					
				Met	His	Pro	Gln	Gln	Leu	Val						
				1					5							
atc	tcc	tgg	ttt	tcc	ctc	gtt	ttg	ctg	gct	tct	ccc	ctc	atg	gcc	ata	222
Ile	Ser	Trp	Phe	Ser	Leu	Val	Leu	Leu	Ala	Ser	Pro	Leu	Met	Ala	Ile	
10						15				20						
tgg	gaa	ctg	gag	aaa	gat	gtt	tat	gtt	gta	gag	ttg	gac	tgg	cac	cct	270
Trp	Glu	Leu	Glu	Lys	Asp	Val	Tyr	Val	Val	Glu	Leu	Asp	Trp	His	Pro	
25						30				35						
gat	gcc	ccc	gga	gaa	atg	gtg	gtc	ctc	acc	tgc	cat	acc	cct	gaa	gaa	318
Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	Thr	Cys	His	Thr	Pro	Glu	Glu	
40						45			50				55			
gat	gac	atc	act	tgg	acc	tca	gct	cag	agc	agt	gaa	gtc	cta	gg	tct	366
Asp	Asp	Ile	Thr	Trp	Thr	Ser	Ala	Gln	Ser	Ser	Glu	Val	Leu	Gly	Ser	
60						65					70					
ggt	aaa	act	ctg	acc	atc	caa	gtc	aaa	gaa	ttt	gga	gat	gct	ggc	cag	414
Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	Glu	Phe	Gly	Asp	Ala	Gly	Gln	
75						80				85						
tat	acc	tgc	cat	aaa	gga	ggc	aag	gtt	ctg	agc	cgc	tca	ctc	ctg	ttg	462
Tyr	Thr	Cys	His	Lys	Gly	Gly	Lys	Val	Leu	Ser	Arg	Ser	Leu	Leu	Leu	

90	95	100	
att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag gaa Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Glu 105	110	115	510
cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag aat Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys Asn 120	125	130	558
tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act gat Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr Asp 140	145	150	606
ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa ggg Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln Gly 155	160	165	654
gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg gac Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val Asp 170	175	180	702
aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt gcc Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser Ala 185	190	195	750
tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat gct Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp Ala 200	205	210	798
att cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc aga Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg 220	225	230	846
gac atc atc aaa cca gac cca ccc aca aac ctg cag ctg aag cca ttg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro Leu 235	240	245	894
aaa aat tct cgg cac gtg gag gtc agc tgg gaa tac ccc gac acc tgg Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp 250	255	260	942
agc acc cca cat tcc tac ttc tcc ctg aca ttt tgc ata cag gcc cag Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala Gln 265	270	275	990
ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag acc Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys Thr 280	285	290	1038
tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa gcc Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln Ala 300	305	310	1086
cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg tcc Arg Asp Arg Tyr Tyr Ser Ser Trp Ser Asp Trp Ala Ser Val Ser 315	320	325	1134

tgc agt taggttccac ccccaggatg aatcttggag ggaaagtgga agatattatg	1190
Cys Ser	
 caaaaatttc taaggacaca ttgaagaggg tccaaaagtt atttctgcc taattttctt	1250
tttgtaaagg gtcattattg tgtcttcgca atatttta catttaaatg ccaaatgccc	1310
actgaaacaa tcagctactt tatTTataga ttTCAGCTA gcaggctgcc actgaccta	1370
atgctattta aatatttaag taatTTatgt atttattaat ttattgttat tgaacacttg	1430
tgtCCAAGA tatATTGAT gttcataacc ctcaggacct gatctgtaag gaataggccc	1490
tattatgcaa aatgtgaatt tatgtgttat ttatactgac aactttcaa gcaagaatgt	1550
atcattttta tgacaaccag tgagcacaca atattatgat gccagcacca taatataattt	1610
gtgatggatg ggaacacaga ggtagttaaa tagagacatg gagacacgaa tccatttgag	1670
aagtttctgg agacggagat gttagatcct gtatccataa agacttcctt gcgggtggtgt	1730
tgataaaagca attcaggggcc acttgcattt ttaagcaagt tttagttttg gatgcctgaa	1790
tttagaaaga cctgagacaa ataactcaa ttgagattca gcttcagcca cttgccagt	1850
ccccatcccc atctatctgt aagtcattgg agagtaccc agggacactg taagtgtctg	1910
gaagtaaaaaa ggtcttatga tccaagaggg agaaccaaca tggccaagca caaaaaattt	1970
tcagaatttc cagctgctcc ttaatagcca ggcaaaaaaa gcacatggat gcaaaagaaaa	2030
tggcaagaa ttgcttactg gacagcgcaa gtgaacctga ctgggtggatg tgaccagaaa	2090
gtgccaatcg ctgaggtgct acttttaagt aatgaatgtg ctttctgtaa agtgatttca	2150
tttctttct gtttacttat ttgttttgc attctgacaa tgcactaata aaaatataac	2210
tcttgtttgc aataataaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa	2267

<210> 108  
<211> 329  
<212> PRT  
<213> Canis familiaris

<400> 108

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu			
1	5	10	15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val		
20	25	30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln  
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val  
85 90 95

Leu Ser Arg Ser Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg  
145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser  
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro  
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu

260

265

270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser  
325

<210> 109  
<211> 2267  
<212> DNA  
<213> Canis familiaris

<400> 109 tttttttttt tttttttttt tttttttttt tattattgca aacaagagtt 60 atatttttat tagtgcattt tcagaatgca aaaacaaata agtaaacaga aaagaaaatga 120 aatcacttta cagaaagcac attcattact taaaagttagc acctcagcga ttggcacttt 180 ctggtcacat ccaccagtca ggttcacttg cgctgtccag taagcaattc ttgaccattt 240 tctttgcattt catgtgcattt ttttgcctgg ctattaagga gcagctggaa attctgacaa 300 ttttttgtgc ttggccatgt tggttctccc tcttggatca taagacctt ttacttccag 360 acacttacag tgtccctggg tcactctcca atgacttaca gatagatggg gatggggact 420 ggcaagggtgg ctgaagctga atctcaattt gagttatttgc tctcaggtct ttctaaattc 480 aggcatccaa aaactaaact tgctaaaaaa tgcaagtggc cctgaattgc ttttatcaaca 540 ccaccgcaag gaagtcttta tggatacagg atctaacatc tccgtctcca gaaacttctc 600 aatatggatttgc gtgtctccat gtctcttattt aactacctct gtgttcccat ccatcacaaa 660 tatattatgg tgctggcatttcaataatattgt gtgctcactg gttgtcataaa aaatgataca 720 ttcttgcttgc aaaagttgtc agtataaata acacataaat tcacattttgc cataataggg 780 cctattcatttcaataatattgt gtgctcactg gttgtcataaa aaatgataca 840 gtgttcaata acaataaaatttcaataatattgt gtgctcactg gttgtcataaa aaatgataca 900 ggtcagtgcc agcctgcttag ctgaaaatct ataaataaaag tagctgatttgc tttcagtgcc 960

catttggcat	ttaaatgtaa	aaaatattgc	gaagacacaa	taatgaccct	ttacaaaaag	1020
aaaatttaggc	agaaaataac	tttgagcc	tcttcaatgt	gtccttagaa	aattttgcat	1080
aatatcttcc	actttccctc	caagattcat	cctgggggtg	gaacctaact	gcaggacaca	1140
gatgcccgagt	cgctccagga	tgaactata	tagcggtctc	gggcttgcac	gcggatctt	1200
gcattccttgt	ggcacacgac	cttggctgag	gtcttgc	cgcagagtct	atcttctt	1260
tctctattgt	tcttgcctg	ggcctgtatg	caaaatgtca	gggagaagta	ggaatgtggg	1320
gtgctccagg	tgtcgggta	ttcccagctg	acctccacgt	gccgagaatt	tttcaatggc	1380
ttcagctgca	ggtttgtggg	tgggtctgg	ttgatgatgt	ctctgatgaa	gaagctgctg	1440
gtgtagttt	catacttgag	cttgtgaata	gcatccacca	cgacctcgat	ggtaggctc	1500
tcctcggcag	aggggcaggc	actgcctcc	tgacactcca	ctgtgtactt	cttataatcc	1560
ctgttgc	ctctgaccct	ctctgctgaa	agtgtcactg	ctccacatgt	cacccttgg	1620
gggtcagaga	agcctctgct	actttgaca	ctgaatttca	aatcagtact	gattgccgtc	1680
agccaccagc	atgtgaaacg	tccagaataa	ttcttcgcct	cacatttcag	aaagatctt	1740
tttttggatt	ctttctgttc	cttaagata	tcagtggacc	aaattccatc	ttctttttg	1800
tgaatcaaca	ggagtgagcg	gctcagaacc	ttgcctc	tatggcaggt	atactggcca	1860
gcatctccaa	attcttgac	ttggatggtc	agagtttac	cagaacctag	gacttcactg	1920
ctctgcgtg	aggtccaagt	gatgtcatct	tcttcagg	tatggcaggt	gaggaccacc	1980
atttctccgg	gggcattcagg	gtgccagtcc	aactctacaa	cataaacatc	tttctccagt	2040
tcccatatgg	ccatgagggg	agacgccagc	aaaacgaggg	aaaaccagga	gatgaccaac	2100
tgctgaggat	gcatcttgct	tctggccagg	ctgcaagg	ccctgggtct	gaaacggagt	2160
ctcctgctgc	tgctgctact	gctactggag	cttatataacc	ctactcctac	cgagctttg	2220
gatggaaact	taaactagaa	actgacttgt	ccaagttgcc	tcgtgcc		2267

<210> 110  
 <211> 7  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Linker

<400> 110

Gly Gly Gly Gly Gly Ser  
1 5

<210> 111  
<211> 10  
<212> PRT  
<213> *Felis catus*

<400> 111

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro  
1               5                           10